

Appendix A1

Applicants copy

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OM protein - protein search, using SW model

Run on: December 25, 2004, 05:24:29 ; Search time 71 Seconds
(without alignments)
1229.090 Million cell updates/sec

Title: US-10-063-734-122

Perfect score: 1301

Sequence: 1 MRPOGPASPORTLIGLLLL.....GDASTGMSVSRILIEELPK 243

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1595201 seqs, 359116952 residues

Total number of hits satisfying chosen parameters: 1595201

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database :
- 1: Published Applications AA.*
 - 2: /cgn2_6/ptodata/1/pubppa/US07_PUBCOMB.pep.*
 - 3: /cgn2_6/ptodata/1/pubppa/US06_PUBCOMB.pep.*
 - 4: /cgn2_6/ptodata/1/pubppa/US05_PUBCOMB.pep.*
 - 5: /cgn2_6/ptodata/1/pubppa/US04_PUBCOMB.pep.*
 - 6: /cgn2_6/ptodata/1/pubppa/US03_PUBCOMB.pep.*
 - 7: /cgn2_6/ptodata/1/pubppa/US02_PUBCOMB.pep.*
 - 8: /cgn2_6/ptodata/1/pubppa/US01_PUBCOMB.pep.*
 - 9: /cgn2_6/ptodata/1/pubppa/US00_PUBCOMB.pep.*
 - 10: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.pep.*
 - 11: /cgn2_6/ptodata/1/pubppa/US08_PUBCOMB.pep.*
 - 12: /cgn2_6/ptodata/1/pubppa/US07_PUBCOMB.pep.*
 - 13: /cgn2_6/ptodata/1/pubppa/US06_PUBCOMB.pep.*
 - 14: /cgn2_6/ptodata/1/pubppa/US05_PUBCOMB.pep.*
 - 15: /cgn2_6/ptodata/1/pubppa/US04_PUBCOMB.pep.*
 - 16: /cgn2_6/ptodata/1/pubppa/US03_PUBCOMB.pep.*
 - 17: /cgn2_6/ptodata/1/pubppa/US02_PUBCOMB.pep.*
 - 18: /cgn2_6/ptodata/1/pubppa/US01_PUBCOMB.pep.*
 - 19: /cgn2_6/ptodata/1/pubppa/US00_PUBCOMB.pep.*
 - 20: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARYS

Result No.	Score	Query Match Length	ID	Description
1	1301	100.0	243 9 US-09-834-759-514	Sequence 514, App
2	1301	100.0	243 10 US-09-938-418-7	Sequence 7, Appl
3	1301	100.0	243 10 US-09-946-374-352	Sequence 352, App
4	1301	100.0	243 10 US-09-946-374-431	Sequence 431, App
5	1301	100.0	243 13 US-10-006-867-122	Sequence 122, App
6	1301	100.0	243 13 US-10-052-586-366	Sequence 366, App
7	1301	100.0	243 13 US-10-007-805-514	Sequence 514, App
8	1301	100.0	243 13 US-10-063-547-122	Sequence 122, App
9	1301	100.0	243 13 US-10-063-551-122	Sequence 122, App
10	1301	100.0	243 14 US-10-174-590-366	Sequence 366, App
11	1301	100.0	243 14 US-10-176-758-366	Sequence 366, App
12	1301	100.0	243 14 US-10-175-737-366	Sequence 366, App
13	1301	100.0	243 14 US-10-063-616-122	Sequence 122, App

14	1301	100.0	243 14	US-10-174-581-366	Sequence 366, App
15	1301	100.0	243 14	US-10-176-483-366	Sequence 366, App
16	1301	100.0	243 14	US-10-176-749-366	Sequence 366, App
17	1301	100.0	243 14	US-10-176-914-366	Sequence 366, App
18	1301	100.0	243 14	US-10-176-915-366	Sequence 366, App
19	1301	100.0	243 14	US-10-063-569-122	Sequence 122, App
20	1301	100.0	243 14	US-10-063-513-122	Sequence 122, App
21	1301	100.0	243 14	US-10-063-515-122	Sequence 122, App
22	1301	100.0	243 14	US-10-063-512-122	Sequence 122, App
23	1301	100.0	243 14	US-10-173-706-366	Sequence 366, App
24	1301	100.0	243 14	US-10-175-728-366	Sequence 366, App
25	1301	100.0	243 14	US-10-175-752-366	Sequence 366, App
26	1301	100.0	243 14	US-10-176-482-366	Sequence 366, App
27	1301	100.0	243 14	US-10-176-757-366	Sequence 366, App
28	1301	100.0	243 14	US-10-176-913-366	Sequence 366, App
29	1301	100.0	243 14	US-10-180-552-366	Sequence 366, App
30	1301	100.0	243 14	US-10-180-557-366	Sequence 366, App
31	1301	100.0	243 14	US-10-076-622-514	Sequence 514, App
32	1301	100.0	243 14	US-10-063-502-122	Sequence 122, App
33	1301	100.0	243 14	US-10-173-700-366	Sequence 366, App
34	1301	100.0	243 14	US-10-173-572-366	Sequence 366, App
35	1301	100.0	243 14	US-10-174-579-366	Sequence 366, App
36	1301	100.0	243 14	US-10-174-582-366	Sequence 366, App
37	1301	100.0	243 14	US-10-174-588-366	Sequence 366, App
38	1301	100.0	243 14	US-10-175-739-366	Sequence 366, App
39	1301	100.0	243 14	US-10-175-740-366	Sequence 366, App
40	1301	100.0	243 14	US-10-175-743-366	Sequence 366, App
41	1301	100.0	243 14	US-10-176-488-366	Sequence 366, App
42	1301	100.0	243 14	US-10-176-482-366	Sequence 366, App
43	1301	100.0	243 14	US-10-176-747-366	Sequence 366, App
44	1301	100.0	243 14	US-10-176-750-366	Sequence 366, App
45	1301	100.0	243 14	US-10-176-985-366	Sequence 366, App

ALIGNMENTS

RESULT 1
US-09-834-759-514
Sequence 514, Application US/09834759
Publication No. US2002008598A1
GENERAL INFORMATION:
APPLICANT: Jians, Yulin
APPLICANT: Dillon, David C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Xu, Jianshun
APPLICANT: Harlocker, Susan L.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.470C9
CURRENT APPLICATION NUMBER: US/09/834,759
CURRENT FILING DATE: 2001-04-13
NUMBER OF SEQ ID NOS: 547
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 514
LENGTH: 243
TYPE: PRT
ORGANISM: Homo sapiens
US-09-834-759-514

Query Match 100.0% Score 1301; DB 9; Length 243;
Best Local Similarity 100.0%; Pred. No. 3e-118;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPOGPASPORTLIGLLLLQLPAPSSASIPKQKQAROREVVDLYNGMCIQGP 60
DB 1 MRPOGPASPORTLIGLLLLQLPAPSSASIPKQKQAROREVVDLYNGMCIQGP 60
QY 61 GVPGRDGSFQANVIFPTPGIPGRDGFKGKGCLEBSFESWTPTNYKQCSNLYGIDL 120
DB 61 GVPGRDGSFQANVIFPTPGIPGRDGFKGKGCLEBSFESWTPTNYKQCSNLYGIDL 120

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QY 121 GKIARCTFTKRSNSALRVLPSSGLRLKCRNACCCORWYFTNGACSGPLPEIAIYYDQ 180
DB 121 GKIARCTFTKRSNSALRVLPSSGLRLKCRNACCCORWYFTNGACSGPLPEIAIYYDQ 180
QY 181 GSPENSTINIRHTSSVEGLCEGIGAGLVDAIIVWGTCSDPYKGDASTGMSVSRITIEE 240
DB 181 GSPENSTINIRHTSSVEGLCEGIGAGLVDAIIVWGTCSDPYKGDASTGMSVSRITIEE 240

PRIOR APPLICATION NUMBER: PCT/US01/21735
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 10
SEQ ID NO 7
LENGTH: 243
TYPE: PRT
ORGANISM: Homo sapien
US-09-938-418-7

Query Match 100.0%; Score 1301; DB 9; Length 243;
Best Local Similarity 100.0%; Pred. No. 3e-118;
Matches .243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 241 LPK 243

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DB 1 MRPGAPASPORAGLILILILLOLPAPSSASEIRKQKQOLRREVVDTLYNGCLOSPA 60
QY 61 GVPGRDPSPGANVLPFTPGIPGRDGFKEGKECELRSEFEESWTNNYKQCSWSIANYGIDL 120
DB 61 GVPGRDPSPGANVLPFTPGIPGRDGFKEGKECELRSEFEESWTNNYKQCSWSIANYGIDL 120
QY 121 GKIARCTFTKRSNSALRVLPSSGLRLKCRNACCCORWYFTNGACSGPLPEIAIYYDQ 180
DB 121 GKIARCTFTKRSNSALRVLPSSGLRLKCRNACCCORWYFTNGACSGPLPEIAIYYDQ 180
QY 181 GSPENSTINIRHTSSVEGLCEGIGAGLVDAIIVWGTCSDPYKGDASTGMSVSRITIEE 240
DB 181 GSPENSTINIRHTSSVEGLCEGIGAGLVDAIIVWGTCSDPYKGDASTGMSVSRITIEE 240
QY 241 LPK 243
DB 241 LPK 243

RESULT 3
US-09-946-374-352
Sequence 352, Application US/09946374
Publication No. US20030073129A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deamoeyers, Luc
APPLICANT: Batton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Collin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830P1C1
CURRENT APPLICATION NUMBER: US/09/946,374
CURRENT FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: 60/098716
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098723
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098749
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098750
PRIOR FILING DATE: 1998-09-01

RESULT 2
US-09-938-418-7
Sequence 7, Application US/09938418
GENERAL INFORMATION:
APPLICANT: Aebkenazl, Avi J.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Gurney, Austin L.
APPLICANT: Polakis, Paul
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Wu, Thomas D.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TITLE OF INVENTION: TREATMENT OF TUMOR
FILE REFERENCE: P5009R1
CURRENT APPLICATION NUMBER: US/09/938,418
CURRENT FILING DATE: 2001-08-23
PRIOR APPLICATION NUMBER: 60/081,071
PRIOR FILING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: 60/085,697
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/097,022
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/101,922
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/103,679
PRIOR FILING DATE: 1998-10-08
PRIOR APPLICATION NUMBER: PCT/US99/05028
PRIOR FILING DATE: 1998-03-08
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: 1999-06-02
PRIOR APPLICATION NUMBER: PCT/US99/20111
PRIOR FILING DATE: 1999-09-01
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US00/04342
PRIOR FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/US00/04341
PRIOR FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: PCT/US01/17800
PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: PCT/US01/19692
PRIOR FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: PCT/US01/21066
PRIOR FILING DATE: 2001-06-29

QY 1 MRPGAPASPORAGLILILILLOLPAPSSASEIRKQKQOLRREVVDTLYNGCLOSPA 60
DB 1 MRPGAPASPORAGLILILILLOLPAPSSASEIRKQKQOLRREVVDTLYNGCLOSPA 60
QY 61 GVPGRDPSPGANVLPFTPGIPGRDGFKEGKECELRSEFEESWTNNYKQCSWSIANYGIDL 120
DB 61 GVPGRDPSPGANVLPFTPGIPGRDGFKEGKECELRSEFEESWTNNYKQCSWSIANYGIDL 120
QY 121 GKIARCTFTKRSNSALRVLPSSGLRLKCRNACCCORWYFTNGACSGPLPEIAIYYDQ 180
DB 121 GKIARCTFTKRSNSALRVLPSSGLRLKCRNACCCORWYFTNGACSGPLPEIAIYYDQ 180
QY 181 GSPENSTINIRHTSSVEGLCEGIGAGLVDAIIVWGTCSDPYKGDASTGMSVSRITIEE 240
DB 181 GSPENSTINIRHTSSVEGLCEGIGAGLVDAIIVWGTCSDPYKGDASTGMSVSRITIEE 240
QY 241 LPK 243
DB 241 LPK 243

RESULT 3
US-09-946-374-352
Sequence 352, Application US/09946374
Publication No. US20030073129A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deamoeyers, Luc
APPLICANT: Batton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
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APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
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PRIOR FILING DATE: 1998-09-01

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Title: US-10-063-734-122

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6: /cgn2_6/ptodata/1/pubppa/US08_NEW_PUB.pep:*
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10: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep:*
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17: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep:*
18: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep:*
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20: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep:*

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SUMMARIES

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2	1301	100.0	243	9	US-09-938-418-7
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9	1301	100.0	243	13	US-10-063-551-122
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42	1301	100.0	243	14	US-10-176-747-366	Sequence 366, App
43	1301	100.0	243	14	US-10-176-750-366	Sequence 366, App
44	1301	100.0	243	14	US-10-176-985-366	Sequence 366, App
45	1301	100.0	243	14	US-10-176-985-366	Sequence 366, App

ALIGNMENTS

RESULT 1
US-09-834-759-514
; Sequence 514, Application US/09834759
; Publication No. US20020085998A1
; GENERAL INFORMATION:
; APPLICANT: Jilang, Yulin
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jianshun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C9
; CURRENT APPLICATION NUMBER: US/09/834,759
; CURRENT FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: PaedSeq for Windows Version 3.0
; SEQ ID NO 514
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-834-759-514

Query Match 100.0%; Score 1301; DB 9; Length 243;
Best Local Similarity 100.0%; Pred. No. 3e-118;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRPGPASPQRRLGILLULLQLPAPSSASIPKQKQAKQROREVDVLYNGMCLQGPA 60
DB 1 MRPGPASPQRRLGILLULLQLPAPSSASIPKQKQAKQROREVDVLYNGMCLQGPA 60
QY 61 GVPGRDPSGANVITPCTPPIGRDGFKEGKECLRESFESWTVPYKQCSWSLNYGIDL 120
DB 61 GVPGRDPSGANVITPCTPPIGRDGFKEGKECLRESFESWTVPYKQCSWSLNYGIDL 120

QY 121 GKIACFTTKRMSNSALRVLFSSGLRLKCRNACCCORWTFNAGACSGPLPIEAIYYDQ 180
 Db 121 GKIACFTTKRMSNSALRVLFSSGLRLKCRNACCCORWTFNAGACSGPLPIEAIYYDQ 180
 QY 181 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIIVWGTCSDPKGDASTGMNSVSRITIEE 240
 Db 181 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIIVWGTCSDPKGDASTGMNSVSRITIEE 240
 QY 241 LPK 243
 Db 241 LPK 243

RESULT 2

US-09-938-418-7
 ; Sequence 7, Application US/09938418
 ; Patent No. US20020161199A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Polakis, Paul
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
 ; FILE OF INVENTION: TREATMENT OF TUMOR
 ; FILE REFERENCE: P5009R1
 ; CURRENT APPLICATION NUMBER: US/09/938, 418
 ; PRIOR FILING DATE: 2001-08-23
 ; PRIOR APPLICATION NUMBER: 60/081, 071
 ; PRIOR FILING DATE: 1998-04-07
 ; PRIOR APPLICATION NUMBER: 60/085, 697
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/097, 022
 ; PRIOR FILING DATE: 1998-08-18
 ; PRIOR APPLICATION NUMBER: 60/101, 922
 ; PRIOR FILING DATE: 1998-09-24
 ; PRIOR APPLICATION NUMBER: 60/103, 679
 ; PRIOR FILING DATE: 1998-10-08
 ; PRIOR APPLICATION NUMBER: PCT/US99/05028
 ; PRIOR FILING DATE: 1999-03-08
 ; PRIOR APPLICATION NUMBER: PCT/US99/12252
 ; PRIOR FILING DATE: 1999-06-02
 ; PRIOR APPLICATION NUMBER: PCT/US99/20111
 ; PRIOR FILING DATE: 1999-09-01
 ; PRIOR APPLICATION NUMBER: PCT/US99/28565
 ; PRIOR FILING DATE: 1999-12-02
 ; PRIOR APPLICATION NUMBER: PCT/US00/04342
 ; PRIOR FILING DATE: 2000-02-18
 ; PRIOR APPLICATION NUMBER: PCT/US00/04341
 ; PRIOR FILING DATE: 2000-02-18
 ; PRIOR APPLICATION NUMBER: PCT/US00/05841
 ; PRIOR FILING DATE: 2000-03-02
 ; PRIOR APPLICATION NUMBER: PCT/US00/08439
 ; PRIOR FILING DATE: 2000-03-30
 ; PRIOR APPLICATION NUMBER: PCT/US00/14042
 ; PRIOR FILING DATE: 2000-05-22
 ; PRIOR APPLICATION NUMBER: PCT/US00/23338
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: PCT/US00/32678
 ; PRIOR FILING DATE: 2000-12-01
 ; PRIOR APPLICATION NUMBER: PCT/US01/06520
 ; PRIOR FILING DATE: 2001-02-28
 ; PRIOR APPLICATION NUMBER: PCT/US01/17800
 ; PRIOR FILING DATE: 2001-06-01
 ; PRIOR APPLICATION NUMBER: PCT/US01/19692
 ; PRIOR FILING DATE: 2001-06-20
 ; PRIOR APPLICATION NUMBER: PCT/US01/21066
 ; PRIOR FILING DATE: 2001-06-29

;; PRIOR APPLICATION NUMBER: PCT/US01/21735
 ;; PRIOR FILING DATE: 2001-07-09
 ;; NUMBER OF SEQ ID NOS: 10
 ;; SEQ ID NO 7
 ;; LENGTH: 243
 ;; TYPE: PRT
 ;; ORGANISM: Homo Sapien
 US-09-938-418-7

Query Match 100.0%; Score 1301; DB 9; Length 243;
 Best Local Similarity 100.0%; Pred. No. 3e-118;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPOGPASPORLRLGLLLLLLOLPAPSSASEIFKQKQKOLQREVDLYNMCIOGPA 60
 Db 1 MRPOGPASPORLRLGLLLLLLOLPAPSSASEIFKQKQKOLQREVDLYNMCIOGPA 60
 QY 61 GVRGRDGSFGANVIFGTGIFGRDGFKEGKECECLRESFESWTPNTKQCSMSLNYGIDL 120
 Db 61 GVRGRDGSFGANVIFGTGIFGRDGFKEGKECECLRESFESWTPNTKQCSMSLNYGIDL 120
 QY 121 GKIACFTTKRMSNSALRVLFSSGLRLKCRNACCCORWTFNAGACSGPLPIEAIYYDQ 180
 Db 121 GKIACFTTKRMSNSALRVLFSSGLRLKCRNACCCORWTFNAGACSGPLPIEAIYYDQ 180
 QY 181 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIIVWGTCSDPKGDASTGMNSVSRITIEE 240
 Db 181 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIIVWGTCSDPKGDASTGMNSVSRITIEE 240
 QY 241 LPK 243
 Db 241 LPK 243

RESULT 3

US-09-946-374-352
 ; Sequence 352, Application US/09946374
 ; Publication No. US20030073129A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Boctstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: P2830P1C1
 ; CURRENT APPLICATION NUMBER: US/09/946, 374
 ; PRIOR FILING DATE: 2001-09-04
 ; PRIOR APPLICATION NUMBER: 60/098716
 ; PRIOR FILING DATE: 1998-09-01
 ; PRIOR APPLICATION NUMBER: 60/098723
 ; PRIOR FILING DATE: 1998-09-01
 ; PRIOR APPLICATION NUMBER: 60/098749
 ; PRIOR FILING DATE: 1998-09-01
 ; PRIOR APPLICATION NUMBER: 60/098750
 ; PRIOR FILING DATE: 1998-09-01


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PRIOR APPLICATION NUMBER: 60/104987
PRIOR FILING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: 60/105000
PRIOR FILING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: 60/105002
PRIOR FILING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: 60/105104
PRIOR FILING DATE: 1998-10-21
PRIOR APPLICATION NUMBER: 60/105169
PRIOR FILING DATE: 1998-10-22
PRIOR APPLICATION NUMBER: 60/105266
PRIOR FILING DATE: 1998-10-22
PRIOR APPLICATION NUMBER: 60/105693
PRIOR FILING DATE: 1998-10-26
PRIOR APPLICATION NUMBER: 60/105694
PRIOR FILING DATE: 1998-10-26
PRIOR APPLICATION NUMBER: 60/105807

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Query Match 100.0%; Score 1301; DB 10; Length 243;
Best Local Similarity 100.0%; Pred. No. 3e-118;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MRPGAPASPOLRGLLILLLOLPAPSSASEIRKQKOLRREVVLDYNGKLOGPA 60
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QY 61 GVRGRDSSPGANVPGTPTGIPGRDQFKGKCELRSEFESWTPNYKQCSMSLNYGIDL 120
Db 61 GVRGRDSSPGANVPGTPTGIPGRDQFKGKCELRSEFESWTPNYKQCSMSLNYGIDL 120
QY 121 GKIACTFTKRSNSALRVFSGSLRLKCRNACCORRYFFNAGCGPPIPAIYYLQ 180
Db 121 GKIACTFTKRSNSALRVFSGSLRLKCRNACCORRYFFNAGCGPPIPAIYYLQ 180
QY 181 GSEPMNSTIHTSTSVGLCEGIGAGLYVVAIIVGTCSDPYKGDASTGNVSRIITIE 240
Db 181 GSEPMNSTIHTSTSVGLCEGIGAGLYVVAIIVGTCSDPYKGDASTGNVSRIITIE 240
QY 241 LPK 243
Db 241 LPK 243

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RESULT 4

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US-09-946-374-431
Sequence 431, Application US/09946374
Publication No. US20030073129A1

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GENERAL INFORMATION:

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APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Batton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Gidwal, Paul J.
APPLICANT: Gurney, Christopher J.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas P.
APPLICANT: Roy, Margaret Ann
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2830P1C1
CURRENT APPLICATION NUMBER: US/09/946,374

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CURRENT FILING DATE: 2001-09-04
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PRIOR FILING DATE: 1998-10-22
PRIOR APPLICATION NUMBER: 60/105266
PRIOR FILING DATE: 1998-10-22
PRIOR APPLICATION NUMBER: 60/105693
PRIOR FILING DATE: 1998-10-26
PRIOR APPLICATION NUMBER: 60/105694
PRIOR FILING DATE: 1998-10-26
PRIOR APPLICATION NUMBER: 60/105807

Query Match 100.0%; Score 1301; DB 10; Length 243;
Best Local Similarity 100.0%; Pred. No. 3e-118;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MBPQGPASPORLRLGLLLLLQLLPAPSSASRTPKQKQALROREVDLYNGMCLQCPA 60
DB 1 MBPQGPASPORLRLGLLLLLQLLPAPSSASRTPKQKQALROREVDLYNGMCLQCPA 60
QY 61 GVPGRDSPGANVIGTRGIPGRDGFKGKGECLRESFESWTPTYKQCSWSLNVGIDL 120
DB 61 GVPGRDSPGANVIGTRGIPGRDGFKGKGECLRESFESWTPTYKQCSWSLNVGIDL 120
QY 121 GKIAECTFTKMSNSALRYLFGSLRLKCRNACCORWYFTFNGACSGCLPTEAIIYLDQ 180
DB 121 GKIAECTFTKMSNSALRYLFGSLRLKCRNACCORWYFTFNGACSGCLPTEAIIYLDQ 180
QY 181 GSPENNSTINHRTSVBGLCEGAGLVDAIWTGTSDDYKGPASTGMSVSRILIE 240
DB 181 GSPENNSTINHRTSVBGLCEGAGLVDAIWTGTSDDYKGPASTGMSVSRILIE 240
QY 241 LPK 243
DB 241 LPK 243

RESULT 5
US-10-066-867-122
; Sequence 122, Application US/10006867
; Publication No. US20020119130A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerlitsen, Mary B.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Guirney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P323ORIC1
; CURRENT APPLICATION NUMBER: US/10/006,867
; PRIOR APPLICATION NUMBER: 2001-12-06
; PRIOR FILING DATE: 1997-10-29

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1 PRIOR APPLICATION NUMBER: 60/064215
2 PRIOR FILING DATE: 1997-10-29
3 PRIOR APPLICATION NUMBER: 60/082797
4 PRIOR FILING DATE: 1998-04-22
5 PRIOR APPLICATION NUMBER: 60/083495
6 PRIOR FILING DATE: 1998-04-29
7 PRIOR APPLICATION NUMBER: 60/085579
8 PRIOR FILING DATE: 1998-05-15
9 PRIOR APPLICATION NUMBER: 60/087759
10 PRIOR FILING DATE: 1998-06-02
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72 PRIOR FILING DATE: 1998-09-10
73 PRIOR APPLICATION NUMBER: 60/099815

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1	PRIOR FILING DATE: 1998-09-10
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15	PRIOR FILING DATE: 1998-09-22
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25	PRIOR FILING DATE: 1998-09-30
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67	PRIOR FILING DATE: 1999-01-22
68	PRIOR APPLICATION NUMBER: 60/1192
69	PRIOR FILING DATE: 1999-02-09
70	PRIOR APPLICATION NUMBER: 60/1198

APPLICANT: Smith,Victoria
APPLICANT: Matanabe,Colin K.
APPLICANT: Wood,William I.
APPLICANT: Zhang,Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C1
CURRENT APPLICATION NUMBER: US/10/052,586
CURRENT FILING DATE: 2002-01-15
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PRIOR APPLICATION NUMBER: 60/063734
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/063870
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066120
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/066466
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/066772
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/069335
PRIOR FILING DATE: 1997-12-11
PRIOR APPLICATION NUMBER: 60/069425
PRIOR FILING DATE: 1997-12-12
PRIOR APPLICATION NUMBER: 60/069870
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/068017
PRIOR FILING DATE: 1997-12-18
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077652
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079786
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/080107
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080194
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080327
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080333
PRIOR FILING DATE: 1998-04-01

PRIOR APPLICATION NUMBER: 60/081049
 PRIOR FILING DATE: 1998-04-08
 PRIOR APPLICATION NUMBER: 60/081070
 PRIOR FILING DATE: 1998-04-08
 PRIOR APPLICATION NUMBER: 60/081195
 PRIOR FILING DATE: 1998-04-09
 PRIOR APPLICATION NUMBER: 60/081838
 PRIOR FILING DATE: 1998-04-15
 PRIOR APPLICATION NUMBER: 60/082568
 PRIOR FILING DATE: 1998-04-21
 PRIOR APPLICATION NUMBER: 60/082569
 PRIOR FILING DATE: 1998-04-21
 PRIOR APPLICATION NUMBER: 60/082704
 PRIOR FILING DATE: 1998-04-22
 PRIOR APPLICATION NUMBER: 60/082797
 PRIOR FILING DATE: 1998-04-22
 PRIOR APPLICATION NUMBER: 60/083322
 PRIOR FILING DATE: 1998-04-28
 PRIOR APPLICATION NUMBER: 60/083495
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083496
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083499
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083559
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/084366
 PRIOR FILING DATE: 1998-05-05
 PRIOR APPLICATION NUMBER: 60/084414
 PRIOR FILING DATE: 1998-05-06
 PRIOR APPLICATION NUMBER: 60/084639
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084640
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084643
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/085573
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085579
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085580
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085582
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085700
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/086023
 PRIOR FILING DATE: 1998-05-18
 PRIOR APPLICATION NUMBER: 60/086392
 PRIOR FILING DATE: 1998-05-22
 PRIOR APPLICATION NUMBER: 60/086486
 PRIOR FILING DATE: 1998-05-22
 PRIOR APPLICATION NUMBER: 60/087098
 PRIOR FILING DATE: 1998-05-28
 PRIOR APPLICATION NUMBER: 60/087208
 PRIOR FILING DATE: 1998-05-28
 PRIOR APPLICATION NUMBER: 60/087609
 PRIOR FILING DATE: 1998-06-02
 PRIOR APPLICATION NUMBER: 60/087759
 PRIOR FILING DATE: 1998-06-02
 PRIOR APPLICATION NUMBER: 60/087827
 PRIOR FILING DATE: 1998-06-03
 PRIOR APPLICATION NUMBER: 60/088025
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088028
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088029
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088033
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088167
 PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/088202

PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/088212
 PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/088217
 PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/088326
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088655
 PRIOR FILING DATE: 1998-06-09
 PRIOR APPLICATION NUMBER: 60/088722
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088738
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088740
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088811
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088824
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088825
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088826
 PRIOR FILING DATE: 1998-06-11
 PRIOR APPLICATION NUMBER: 60/088861
 PRIOR FILING DATE: 1998-06-11
 PRIOR APPLICATION NUMBER: 60/088863
 PRIOR FILING DATE: 1998-06-11
 PRIOR APPLICATION NUMBER: 60/088876
 PRIOR FILING DATE: 1998-06-11
 PRIOR APPLICATION NUMBER: 60/089090
 PRIOR FILING DATE: 1998-06-12
 PRIOR APPLICATION NUMBER: 60/089105
 PRIOR FILING DATE: 1998-06-12
 PRIOR APPLICATION NUMBER: 60/089512
 PRIOR FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: 60/089514
 PRIOR FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: 60/089538
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089598
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089653
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089908

Query Match 100.0%; Score 1301; DB 13; Length 243;
 Best Local Similarity 100.0%; Pred. No. 3e-118;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPGPASPORLRLGLLLLLQLPAPASAEIRKQKQKOLQREBYVLDLYNCKLOGPA 60
 DB 1 MRPGPASPORLRLGLLLLLQLPAPASAEIRKQKQKOLQREBYVLDLYNCKLOGPA 60
 QY 61 GVGGRDSSPGANVIRGTGIGIRGDFGKGECELRSEFESWTPNKKQCSWSLWYIDL 120
 DB 61 GVGGRDSSPGANVIRGTGIGIRGDFGKGECELRSEFESWTPNKKQCSWSLWYIDL 120
 QY 121 GKIACTFTKRSNSALRVLFSSGLRLKCRNACCOMWTFNCAECSGLPTEAITIYDQ 180
 DB 121 GKIACTFTKRSNSALRVLFSSGLRLKCRNACCOMWTFNCAECSGLPTEAITIYDQ 180
 QY 161 GSPENSTINIRHRSVVEGICGEGIGAGLVDAIWTGTCSDYPRKGDASTGMSVSRITIEE 240
 DB 161 GSPENSTINIRHRSVVEGICGEGIGAGLVDAIWTGTCSDYPRKGDASTGMSVSRITIEE 240
 QY 241 LPK 243
 DB 241 LPK 243

RESULT 7
 US-10-007-805-514
 Sequence 514, Application US/10007805

QY 181 GSPENNSTINIRHTSSVEGLCEGIGAGLVDAIWMGTCSDPKGDASTGMNSVSRIIIEE 240
 Db 181 GSPENNSTINIRHTSSVEGLCEGIGAGLVDAIWMGTCSDPKGDASTGMNSVSRIIIEE 240
 QY 241 LPK 243
 Db 241 LPK 243

RESULT 10
 US-10-174-590-366
 ; Sequence 366, Application US/10174590
 ; Publication No. US20030008352A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jlan
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Pan, James
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3430R1C42
 ; CURRENT APPLICATION NUMBER: US/10/174,590
 ; PRIOR APPLICATION DATE: 2002-06-18
 ; PRIOR APPLICATION REMOVED - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 612
 ; SEQ ID NO 366
 ; LENGTH: 243
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 ; US-10-174-590-366

Query Match 100.0%; Score 1301; DB 14; Length 243;
 Best Local Similarity 100.0%; Pred. No. 3e-118;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRPOGPASPORLRLGILLILLIQLPAPSSASEIPKQKQAKLRQREVDVLYNGMCLQCPA 60
 Db 1 MRPOGPASPORLRLGILLILLIQLPAPSSASEIPKQKQAKLRQREVDVLYNGMCLQCPA 60
 QY 61 GVPGRDPSGANVIGTGTGIPGRDGFKEGKGLRESFEESWTNPKKOCSSSLNYGIDL 120
 Db 61 GVPGRDPSGANVIGTGTGIPGRDGFKEGKGLRESFEESWTNPKKOCSSSLNYGIDL 120
 QY 121 GKIAECTTKRNSALRVLFSGSLRLKCRNACCORWYFTFNAGCSPPLPIEATIIYDQ 180
 Db 121 GKIAECTTKRNSALRVLFSGSLRLKCRNACCORWYFTFNAGCSPPLPIEATIIYDQ 180
 QY 181 GSPENNSTINIRHTSSVEGLCEGIGAGLVDAIWMGTCSDPKGDASTGMNSVSRIIIEE 240
 Db 181 GSPENNSTINIRHTSSVEGLCEGIGAGLVDAIWMGTCSDPKGDASTGMNSVSRIIIEE 240
 QY 241 LPK 243
 Db 241 LPK 243

RESULT 11
 US-10-176-758-366
 ; Sequence 366, Application US/10176758
 ; Publication No. US20030008353A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jlan
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; US-10-176-758-366

APPLICANT: Gurney, Austin L.
 APPLICANT: Pan, James
 APPLICANT: Smith, Victoria
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3430R1C40
 ; CURRENT APPLICATION NUMBER: US/10/176,758
 ; PRIOR APPLICATION DATE: 2002-06-21
 ; PRIOR APPLICATION REMOVED - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 612
 ; SEQ ID NO 366
 ; LENGTH: 243
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 ; US-10-176-758-366

Query Match 100.0%; Score 1301; DB 14; Length 243;
 Best Local Similarity 100.0%; Pred. No. 3e-118;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRPOGPASPORLRLGILLILLIQLPAPSSASEIPKQKQAKLRQREVDVLYNGMCLQCPA 60
 Db 1 MRPOGPASPORLRLGILLILLIQLPAPSSASEIPKQKQAKLRQREVDVLYNGMCLQCPA 60
 QY 61 GVPGRDPSGANVIGTGTGIPGRDGFKEGKGLRESFEESWTNPKKOCSSSLNYGIDL 120
 Db 61 GVPGRDPSGANVIGTGTGIPGRDGFKEGKGLRESFEESWTNPKKOCSSSLNYGIDL 120
 QY 121 GKIAECTTKRNSALRVLFSGSLRLKCRNACCORWYFTFNAGCSPPLPIEATIIYDQ 180
 Db 121 GKIAECTTKRNSALRVLFSGSLRLKCRNACCORWYFTFNAGCSPPLPIEATIIYDQ 180
 QY 181 GSPENNSTINIRHTSSVEGLCEGIGAGLVDAIWMGTCSDPKGDASTGMNSVSRIIIEE 240
 Db 181 GSPENNSTINIRHTSSVEGLCEGIGAGLVDAIWMGTCSDPKGDASTGMNSVSRIIIEE 240
 QY 241 LPK 243
 Db 241 LPK 243

RESULT 12
 US-10-175-737-366
 ; Sequence 366, Application US/10175737
 ; Publication No. US20030013153A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jlan
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Pan, James
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3430R1C50
 ; CURRENT APPLICATION NUMBER: US/10/175,737
 ; PRIOR APPLICATION DATE: 2002-06-19
 ; PRIOR APPLICATION REMOVED - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 612
 ; SEQ ID NO 366
 ; LENGTH: 243
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 ; US-10-175-737-366

Query Match 100.0%; Score 1301; DB 14; Length 243;
Best Local Similarity 100.0%; Pred. No. 3e-118;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPOGPASPORLRLGLLLLLQLPAPSSASEIPKQKQAOUREVVDLYNGMCLQCPA 60
DB 1 MRPOGPASPORLRLGLLLLLQLPAPSSASEIPKQKQAOUREVVDLYNGMCLQCPA 60
QY 61 GVPBGDGSAGANVIGTPTGIPGRDGFKGKGECLRESFESWTPTYKQCSWSLNYGIDL 120
DB 61 GVPBGDGSAGANVIGTPTGIPGRDGFKGKGECLRESFESWTPTYKQCSWSLNYGIDL 120
QY 121 GKIACTFTKMSNSALRYLFGSLRLKCRNACCORWYTFNGACSGPLPIEAIITYLDQ 180
DB 121 GKIACTFTKMSNSALRYLFGSLRLKCRNACCORWYTFNGACSGPLPIEAIITYLDQ 180
QY 181 GSPENNSTINIRHTSSVEGLCEGIGAGLVDAIWTGCSDPYKGDASTGMSVSRIIIEE 240
DB 181 GSPENNSTINIRHTSSVEGLCEGIGAGLVDAIWTGCSDPYKGDASTGMSVSRIIIEE 240
QY 241 LPK 243
DB 241 LPK 243

RESULT 13
US-10-063-616-122
; Sequence 122, Application US/10063616
; Publication No. US20030013855A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Goddard, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063, 616
; PRIOR FILING DATE: 2002-05-03
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 122
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-616-122

Query Match 100.0%; Score 1301; DB 14; Length 243;
Best Local Similarity 100.0%; Pred. No. 3e-118;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPOGPASPORLRLGLLLLLQLPAPSSASEIPKQKQAOUREVVDLYNGMCLQCPA 60
DB 1 MRPOGPASPORLRLGLLLLLQLPAPSSASEIPKQKQAOUREVVDLYNGMCLQCPA 60
QY 61 GVPBGDGSAGANVIGTPTGIPGRDGFKGKGECLRESFESWTPTYKQCSWSLNYGIDL 120
DB 61 GVPBGDGSAGANVIGTPTGIPGRDGFKGKGECLRESFESWTPTYKQCSWSLNYGIDL 120
QY 121 GKIACTFTKMSNSALRYLFGSLRLKCRNACCORWYTFNGACSGPLPIEAIITYLDQ 180
DB 121 GKIACTFTKMSNSALRYLFGSLRLKCRNACCORWYTFNGACSGPLPIEAIITYLDQ 180
QY 181 GSPENNSTINIRHTSSVEGLCEGIGAGLVDAIWTGCSDPYKGDASTGMSVSRIIIEE 240
DB 181 GSPENNSTINIRHTSSVEGLCEGIGAGLVDAIWTGCSDPYKGDASTGMSVSRIIIEE 240
QY 241 LPK 243
DB 241 LPK 243

DB 241 LPK 243

RESULT 14
US-10-174-581-366
; Sequence 366, Application US/10174581
; Publication No. US20030017540A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Goddard, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C41
; CURRENT APPLICATION NUMBER: US/10/174, 581
; PRIOR FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063564
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063734
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/063870
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066120
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/066466
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/066772
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/069335
; PRIOR FILING DATE: 1997-12-11
; PRIOR APPLICATION NUMBER: 60/069425
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: 60/069870
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/068017
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11

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1 PRIOR FILING DATE: 1998-05-28
2 PRIOR APPLICATION NUMBER: 60/087609
3 PRIOR FILING DATE: 1998-06-02
4 PRIOR APPLICATION NUMBER: 60/087759
5 PRIOR FILING DATE: 1998-06-02
6 PRIOR APPLICATION NUMBER: 60/087827
7 PRIOR FILING DATE: 1998-06-03
8 PRIOR APPLICATION NUMBER: 60/088025
9 PRIOR FILING DATE: 1998-06-04
10 PRIOR APPLICATION NUMBER: 60/088028
11 PRIOR FILING DATE: 1998-06-04
12 PRIOR APPLICATION NUMBER: 60/088029
13 PRIOR FILING DATE: 1998-06-04
14 PRIOR APPLICATION NUMBER: 60/088033
15 PRIOR FILING DATE: 1998-06-04
16 PRIOR APPLICATION NUMBER: 60/088167
17 PRIOR FILING DATE: 1998-06-05
18 PRIOR APPLICATION NUMBER: 60/088202
19 PRIOR FILING DATE: 1998-06-05
20 PRIOR APPLICATION NUMBER: 60/088212
21 PRIOR FILING DATE: 1998-06-05
22 PRIOR APPLICATION NUMBER: 60/088217
23 PRIOR FILING DATE: 1998-06-05
24 PRIOR APPLICATION NUMBER: 60/088326
25 PRIOR FILING DATE: 1998-06-04
26 PRIOR APPLICATION NUMBER: 60/088655
27 PRIOR FILING DATE: 1998-06-09
28 PRIOR APPLICATION NUMBER: 60/088722
29 PRIOR FILING DATE: 1998-06-10
30 PRIOR APPLICATION NUMBER: 60/088738
31 PRIOR FILING DATE: 1998-06-10
32 PRIOR APPLICATION NUMBER: 60/088740
33 PRIOR FILING DATE: 1998-06-10
34 PRIOR APPLICATION NUMBER: 60/088811
35 PRIOR FILING DATE: 1998-06-10
36 PRIOR APPLICATION NUMBER: 60/088824
37 PRIOR FILING DATE: 1998-06-10
38 PRIOR APPLICATION NUMBER: 60/088825
39 PRIOR FILING DATE: 1998-06-10
40 PRIOR APPLICATION NUMBER: 60/088826
41 PRIOR FILING DATE: 1998-06-10
42 PRIOR APPLICATION NUMBER: 60/088861
43 PRIOR FILING DATE: 1998-06-11
44 PRIOR APPLICATION NUMBER: 60/088863
45 PRIOR FILING DATE: 1998-06-11
46 PRIOR APPLICATION NUMBER: 60/088876
47 PRIOR FILING DATE: 1998-06-11
48 PRIOR APPLICATION NUMBER: 60/089090
49 PRIOR FILING DATE: 1998-06-12
50 PRIOR APPLICATION NUMBER: 60/089105
51 PRIOR FILING DATE: 1998-06-12
52 PRIOR APPLICATION NUMBER: 60/089512
53 PRIOR FILING DATE: 1998-06-16
54 PRIOR APPLICATION NUMBER: 60/089514
55 PRIOR FILING DATE: 1998-06-16
56 PRIOR APPLICATION NUMBER: 60/089538
57 PRIOR FILING DATE: 1998-06-17
58 PRIOR APPLICATION NUMBER: 60/089598
59 PRIOR FILING DATE: 1998-06-17
60 PRIOR APPLICATION NUMBER: 60/089653

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Query Match	100.0%	Score 1301	DB 14	Length 243
Best Local Similarity	100.0%	Pred. No. 3e-118		
Matches 243	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	MPQGPAAAPQRLKGLLLILLLOLPAPSSASBP	PKQKQAKOLRQREVVLDYNGMCLQSPA	60
Db	1	MPQGPAAAPQRLKGLLLILLLOLPAPSSASBP	PKQKQAKOLRQREVVLDYNGMCLQSPA	60
QY	61	GVPGDGGSPGANVLPQTPIGIPGRDGFGEAGCECLRES	PESMTPTNYKQCSWSLNYGIDL	120
Db	61	GVPGDGGSPGANVLPQTPIGIPGRDGFGEAGCECLRES	PESMTPTNYKQCSWSLNYGIDL	120

QY 121 GKIAECTFTKRSNSALRYLFGSLRLKCRNACCORWYFTFNGAECGPIPIAIIYLDQ 180
DB 121 GKIAECTFTKRSNSALRYLFGSLRLKCRNACCORWYFTFNGAECGPIPIAIIYLDQ 180
QY 181 GSPENNSTINIHRSSVEGLCEGIGAGLVDAIIVGTCSDYPKDASTGMNSYSRIIIEE 240
DB 181 GSPENNSTINIHRSSVEGLCEGIGAGLVDAIIVGTCSDYPKDASTGMNSYSRIIIEE 240
QY 241 LPK 243
DB 241 LPK 243

RESULT 15

US-10-176-483-366
Sequence 366, Application US/10176483
Publication No. US20030017541A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C68
CURRENT APPLICATION NUMBER: US/10/176,483
CURRENT FILING DATE: 2002-06-20
Prior application removed - See file wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 366
LENGTH: 243
TYPE: PRT
ORGANISM: Homo Sapien
US-10-176-483-366

Query Match 100.0%; Score 1301; DB 14; Length 243;
Best Local Similarity 100.0%; Pred. No. 3e-118;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRQGPASFORLRLGLLLLLQLPAPSSASEIPKQKQALRQREVVDLYNMCLOGPA 60
DB 1 MRQGPASFORLRLGLLLLLQLPAPSSASEIPKQKQALRQREVVDLYNMCLOGPA 60
QY 61 GYVGRDGSFGANVIFGTPIGRDGRKGECECLRSFESWTPTYKQCSWSSLYNGIDL 120
DB 61 GYVGRDGSFGANVIFGTPIGRDGRKGECECLRSFESWTPTYKQCSWSSLYNGIDL 120
QY 121 GKIAECTFTKRSNSALRYLFGSLRLKCRNACCORWYFTFNGAECGPIPIAIIYLDQ 180
DB 121 GKIAECTFTKRSNSALRYLFGSLRLKCRNACCORWYFTFNGAECGPIPIAIIYLDQ 180
QY 181 GSPENNSTINIHRSSVEGLCEGIGAGLVDAIIVGTCSDYPKDASTGMNSYSRIIIEE 240
DB 181 GSPENNSTINIHRSSVEGLCEGIGAGLVDAIIVGTCSDYPKDASTGMNSYSRIIIEE 240
QY 241 LPK 243
DB 241 LPK 243

Search completed: December 25, 2004, 05:29:47
Job time: 73 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 25, 2004, 02:24:05 ; Search time 77 Seconds
(without alignments)
1132.094 Million cell updates/sec

Title: US-10-063-734-122

Perfect score: 1301
Sequence: 1 MRPGPASPQRRLRLLL.....GDASTGWSVSRRIIEELPK 243

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1301	100.0	243	3	AA99462 Human PRO
2	1301	100.0	243	3	AA99441 Human PRO
3	1301	100.0	243	4	AA866130 Protein o
4	1301	100.0	243	4	AA866211 Protein o
5	1301	100.0	243	4	AAU29206 Human PRO
6	1301	100.0	243	4	AA887586 Human PRO
7	1301	100.0	243	5	AB935911 Human sec
8	1301	100.0	243	5	AB884939 Human PRO
9	1301	100.0	243	5	AAE20462 Human tum
10	1301	100.0	243	5	AB935545 Human ang
11	1301	100.0	243	5	ABP68636 Human pan
12	1301	100.0	243	5	ABG78938 Human bre
13	1301	100.0	243	5	ABUS8582 Human PRO
14	1301	100.0	243	6	ABUS8130 Novel hum
15	1301	100.0	243	6	ABUS4445 Human sec
16	1301	100.0	243	6	ABR6319 Human sec
17	1301	100.0	243	6	ABR5709 Human sec
18	1301	100.0	243	6	ABU9649 Human sec
19	1301	100.0	243	6	ABJ37761 Human tum
20	1301	100.0	243	6	ABUS2888 Human PRO
21	1301	100.0	243	6	ABUS0009 Novel hum
22	1301	100.0	243	6	ABR88258 Human sec
23	1301	100.0	243	6	ABU96311 Novel hum
24	1301	100.0	243	6	ABU92742 Human sec
25	1301	100.0	243	6	ABO08819 Human sec

ALIGNMENTS

RESULT 1	AA99462	ABO02871	Human sec
ID	AA99462	ABr75025	Human sec
XX	AA99462;	ABR94787	Human sec
AC	AA99462;	ABR85760	Human PRO
XX	08-AUG-2000 (first entry)	ABU98920	Novel hum
DT	08-AUG-2000 (first entry)	ABU98135	Novel hum
XX	Human PRO1550 amino acid sequence SEQ ID NO:431.	ABU91841	Novel hum
DE	Human PRO1550 amino acid sequence SEQ ID NO:431.	ABU89534	Human PRO
XX	Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;	ABU86375	Human sec
KW	transmembrane; secretion; immunoadhesion; pharmaceutical; screening;	ABR67588	Human sec
XX		ABU80616	Human PRO
OS	Homo sapiens.	ABU90936	Novel hum
XX		ABO33995	Human sec
PN	WO200012708-A2.	ABR99534	Human sec
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XX		ABO16447	Human sec
PF	01-SEP-1999;	ABR92347	Human sec
XX		ABO18988	Human sec
XX		ABR78409	Human sec
XX		ABU72012	Novel hum
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XX	01-SEP-1998;	98US-0098716P.	
PR	01-SEP-1998;	98US-0098749P.	
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PR	02-SEP-1998;	98US-0098803P.	
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PR	10-SEP-1998;	98US-0099792P.	
PR	10-SEP-1998;	98US-0099808P.	
PR	10-SEP-1998;	98US-0099812P.	
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PR	15-SEP-1998;	98US-0100385P.	
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PR	15-SEP-1998;	98US-0100390P.	
PR	16-SEP-1998;	98US-0100584P.	
PR	16-SEP-1998;	98US-0100627P.	
PR	16-SEP-1998;	98US-0100661P.	
PR	16-SEP-1998;	98US-0100662P.	
PR	16-SEP-1998;	98US-0100664P.	

PR 17-SEP-1998; 98US-0100683P.
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 PR 17-SEP-1998; 98US-0100710P.
 PR 17-SEP-1998; 98US-0100711P.
 PR 17-SEP-1998; 98US-0100919P.
 PR 18-SEP-1998; 98US-0100930P.
 PR 18-SEP-1998; 98US-0100848P.
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 PR 22-SEP-1998; 98US-0101272P.
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 PR 01-OCT-1998; 98US-0102644P.
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 PR 02-OCT-1998; 98US-0102656P.
 PR 06-OCT-1998; 98US-0103258P.
 PR 06-OCT-1998; 98US-0103449P.
 PR 07-OCT-1998; 98US-0103314P.
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 PR 14-OCT-1998; 98US-0103711P.
 PR 14-OCT-1998; 98US-0104257P.
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 PR 21-OCT-1998; 98US-0105104P.
 PR 21-OCT-1998; 98US-0105169P.
 PR 22-OCT-1998; 98US-0105266P.
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 PR 27-OCT-1998; 98US-0105881P.
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 PR 28-OCT-1998; 98US-0106023P.
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 PR 28-OCT-1998; 98US-0106029P.
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 PR 28-OCT-1998; 98US-0106032P.
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 PR 28-OCT-1998; 98US-0106178P.
 PR 29-OCT-1998; 98US-0106248P.
 PR 29-OCT-1998; 98US-0106384P.
 PR 30-OCT-1998; 98US-0106500P.
 PR 30-OCT-1998; 98US-0106464P.
 PR 03-NOV-1998; 98US-0106856P.
 PR 03-NOV-1998; 98US-0106902P.

PR 03-NOV-1998; 98US-0106905P.
 PR 03-NOV-1998; 98US-0106919P.
 PR 03-NOV-1998; 98US-0106932P.
 PR 03-NOV-1998; 98US-0106934P.
 PR 10-NOV-1998; 98US-0107783P.
 PR 17-NOV-1998; 98US-0108775P.
 PR 17-NOV-1998; 98US-0108779P.
 PR 17-NOV-1998; 98US-0108787P.
 PR 17-NOV-1998; 98US-0108788P.
 PR 17-NOV-1998; 98US-0108801P.
 PR 17-NOV-1998; 98US-0108802P.
 PR 17-NOV-1998; 98US-0108806P.
 PR 17-NOV-1998; 98US-0108807P.
 PR 17-NOV-1998; 98US-0108867P.
 PR 18-NOV-1998; 98US-0108925P.
 PR 18-NOV-1998; 98US-0108848P.
 PR 18-NOV-1998; 98US-0108849P.
 PR 18-NOV-1998; 98US-0108850P.
 PR 18-NOV-1998; 98US-0108851P.
 PR 18-NOV-1998; 98US-0108852P.
 PR 18-NOV-1998; 98US-0108858P.
 PR 18-NOV-1998; 98US-0108904P.
 PA (GETH) GENENTECH INC.
 XX
 PI Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI,
 XX WPI, 2000-237871/20.
 DR N-PSDB; AAA37144.
 DR XX
 PT New mammalian DNA sequences encoding transmembrane, receptor or secreted
 PT PRO polypeptides, useful for screening of potential peptide or small
 PT molecule inhibitors of the relevant receptor/ligand interactions.
 XX
 PS Claim 12; Fig 246; 773pp; English.
 XX
 CC AAA37022 to AAA37144 encode the new isolated human transmembrane,
 CC receptor or secreted PRO polypeptides given in AA99340 to AA99462. The
 CC transmembrane and receptor PRO proteins can be used for screening of
 CC potential peptide or small molecule inhibitors of the relevant
 CC receptor/ligand interactions. The polypeptides and nucleotide sequences
 CC encoding them have various industrial applications, including uses as
 CC pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR
 CC primers and hybridisation probes used in the isolation of the PRO
 CC polypeptides from the present invention
 XX
 SQ Sequence 243 AA;
 QY Query Match 100.0%; Score 1301; DB 3; Length 243;
 DB Best Local Similarity 100.0%; Pred. No. 3, 2e-121; Mismatches 0; Indels 0; Gaps 0;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRPGAPASPORLRLILLLILQLPAPSSASEIRKQKQKQLRQREVVDLYNMCLOGPA 60
 DB 1 MRPGAPASPORLRLILLLILQLPAPSSASEIRKQKQKQLRQREVVDLYNMCLOGPA 60
 QY 61 GVPGRDGSFGANVLTGTGIPGRDGFGEKGECLRESFEESWTPNKKQCSWSLNGIDL 120
 DB 61 GVPGRDGSFGANVLTGTGIPGRDGFGEKGECLRESFEESWTPNKKQCSWSLNGIDL 120
 QY 121 GKIACTFTKRSNSALRVLFSSGLRLKCRNACCQRYFTFNGABCSGLPIEALIIYDQ 180
 DB 121 GKIACTFTKRSNSALRVLFSSGLRLKCRNACCQRYFTFNGABCSGLPIEALIIYDQ 180
 QY 181 GSPENNSTINIHRTSVEGLCEGIGAGLVNVAITWGTGSDYKGDASTGWSVSIIEE 240
 DB 181 GSPENNSTINIHRTSVEGLCEGIGAGLVNVAITWGTGSDYKGDASTGWSVSIIEE 240
 QY 241 LPK 243
 DB 241 LPK 243

PI Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;
 XX WPI; 2000-237871/20.
 DR N-PSDB; AAA37123.
 XX
 PT New mammalian DNA sequences encoding transmembrane, receptor or secreted
 PT PRO, polypeptides, useful for screening of potential peptide or small
 PT molecule inhibitors of the relevant receptor/ligand interactions.
 XX
 PS Claim 12; Fig 204; 773pp; English.

CC AAA37022 to AAA37144 encode the new isolated human transmembrane,
 CC receptor or secreted PRO polypeptides given in AA99340 to AA99462. The
 CC transmembrane and receptor PRO proteins can be used for screening of
 CC potential peptide or small molecule inhibitors of the relevant
 CC receptor/ligand interactions. The polypeptides and nucleotide sequences
 CC encoding them have various industrial applications, including uses as
 CC pharmaceutical and diagnostic agents. AAA37145 to AAA3730 represent PCR
 CC primers and hybridization probes used in the isolation of the PRO
 CC polypeptides from the present invention

Sequence 243 AA;

Query Match 100.0%; Score 1301; DB 3; Length 243;
 Best Local Similarity 100.0%; Pred. No. 3.2e-121; Mismatches 0; Gaps 0;
 Matches 243; Conservative 0; Indels 0;

QY 1 MRPGPASPQRRLGLLILLLQLPAPSSASIEIPKQKQALRQREVVDLYNMGCLQGPA 60
 DB 1 MRPGPASPQRRLGLLILLLQLPAPSSASIEIPKQKQALRQREVVDLYNMGCLQGPA 60
 QY 61 GVPGRDSSPGANVLPETPGIPGRDGFKEGECRESFEESWTPTYKQCSWSSLYNGIDL 120
 DB 61 GVPGRDSSPGANVLPETPGIPGRDGFKEGECRESFEESWTPTYKQCSWSSLYNGIDL 120
 QY 121 GKIAECTFTKRSNSALRYLFSGLRLKCRNACCORWYFTFNGAECGSLPIEAIYYLDQ 180
 DB 121 GKIAECTFTKRSNSALRYLFSGLRLKCRNACCORWYFTFNGAECGSLPIEAIYYLDQ 180
 QY 181 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIIVGTCSDYPKGDASTGMNSVSRITIEE 240
 DB 181 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIIVGTCSDYPKGDASTGMNSVSRITIEE 240
 QY 241 LPK 243
 DB 241 LPK 243

RESULT 3

AAAB6190 standard; protein; 243 AA.

AAAB6190;
 02-APR-2001 (first entry)

Protein of the invention #102.

Secreted; transmembrane; gene therapy.
 Unidentified.

XX WO200078961-A1.
 PD 28-DEC-2000.
 PF 18-FEB-2000; 2000MO-US004342.
 XX 23-JUN-1999; 99US-0141037P.
 PR 20-JUL-1999; 99US-0144758P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 01-SEP-1999; 99MO-US020111.
 PR 29-OCT-1999; 99US-0162506P.

PR 30-NOV-1999; 99MO-US028313.
 PR 02-DEC-1999; 99MO-US028551.
 PR 16-DEC-1999; 99MO-US03095.
 PR 05-JAN-2000; 2000MO-US000219.
 PR 06-JAN-2000; 2000MO-US000376.
 XX
 PA (GENTH) GENENTECH INC.

PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
 PI Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
 PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
 PI Williams PM, Wood WI;
 DR WPI; 2001-071395/08.

PT Secreted and transmembrane proteins and nucleic acids designated PRO,
 PT useful as hybridization probes, in chromosome and gene mapping and gene
 PT therapy.

Sequence 243 AA;

Query Match 100.0%; Score 1301; DB 4; Length 243;
 Best Local Similarity 100.0%; Pred. No. 3.2e-121; Mismatches 0; Gaps 0;
 Matches 243; Conservative 0; Indels 0;

QY 1 MRPGPASPQRRLGLLILLLQLPAPSSASIEIPKQKQALRQREVVDLYNMGCLQGPA 60
 DB 1 MRPGPASPQRRLGLLILLLQLPAPSSASIEIPKQKQALRQREVVDLYNMGCLQGPA 60
 QY 61 GVPGRDSSPGANVLPETPGIPGRDGFKEGECRESFEESWTPTYKQCSWSSLYNGIDL 120
 DB 61 GVPGRDSSPGANVLPETPGIPGRDGFKEGECRESFEESWTPTYKQCSWSSLYNGIDL 120
 QY 121 GKIAECTFTKRSNSALRYLFSGLRLKCRNACCORWYFTFNGAECGSLPIEAIYYLDQ 180
 DB 121 GKIAECTFTKRSNSALRYLFSGLRLKCRNACCORWYFTFNGAECGSLPIEAIYYLDQ 180
 QY 181 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIIVGTCSDYPKGDASTGMNSVSRITIEE 240
 DB 181 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIIVGTCSDYPKGDASTGMNSVSRITIEE 240
 QY 241 LPK 243
 DB 241 LPK 243

RESULT 4

AAAB6211 standard; protein; 243 AA.

AAAB6211;
 02-APR-2001 (first entry)

Protein of the invention #123.

Secreted; transmembrane; gene therapy.
 Unidentified.

XX WO200078961-A1.
 PD 28-DEC-2000.

XX 18-FEB-2000; 2000MO-US004342.
XX
XX 23-JUN-1999; 99US-0141037P.
XX 20-JUL-1999; 99US-0144758P.
XX 26-JUL-1999; 99US-0145698P.
XX 01-SEP-1999; 99MO-US020111.
XX 29-OCT-1999; 99US-0162506P.
XX 30-NOV-1999; 99MO-US028313.
XX 02-DEC-1999; 99MO-US028551.
XX 16-DEC-1999; 99MO-US030095.
XX 05-JAN-2000; 2000MO-US000219.
XX 06-JAN-2000; 2000MO-US000376.
XX
XX (GETH) GENENTECH INC.
XX
XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S,
XX Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ,
XX Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK,
XX Williams PM, Wood WI,
XX WPI; 2001-071395/08.
XX
XX Secreted and transmembrane proteins and nucleic acids designated PRO,
XX PT useful as hybridization probes, in chromosome and gene mapping and gene
XX therapy.
XX
XX Claim 1; Fig 246; 787bp; English.
XX
XX The present invention relates to secreted and transmembrane proteins.
XX CC These proteins and the DNA encoding them may be used as hybridization
XX CC probes, in chromosome and gene mapping and in the generation of anti-
XX CC sense RNA and DNA. They may also be used to generate either
XX CC transgenic animals or knockout animals which are in turn useful for
XX CC development and screening of therapeutically useful reagents. The nucleic
XX CC acids may also be used in gene therapy
XX
XX Sequence 243 AA;
XX
XX Query Match 100.0%; Score 1301; DB 4; Length 243;
XX Best Local Similarity 100.0%; Pred. No. 3.2e-121;
XX Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 MRRGGAASRPRGILLLILQLPAPSSASEIPKSKOKAQRORVNDLYNMCLOGPA 60
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XX 1 MRRGGAASRPRGILLLILQLPAPSSASEIPKSKOKAQRORVNDLYNMCLOGPA 60
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XX 61 GVPGRDSPGANVYPTGPGIPGRDGFKEGKECECLRESFESWTPTNYKQCSWSLNYGIDL 120
XX |
XX 61 GVPGRDSPGANVYPTGPGIPGRDGFKEGKECECLRESFESWTPTNYKQCSWSLNYGIDL 120
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XX 121 GKIAECTFTMRNSALRVLFSGSLRLKCKNACCQRMWYFTFNGACEGSPLEIAIYLDQ 180
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XX 181 GSPENSTINIHRTSSVEGICGIGLVDAIWNCTGSDYPRGDSATGMSVRIITE 240
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XX 241 LPK 243
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XX 241 LPK 243
XX |
XX
XX RESULT 5
XX AAU29206
XX ID AAU29206 standard; protein; 243 AA.
XX
XX AAU29206;
XX
XX 18-DEC-2001 (first entry)
XX
XX Human PRO polypeptide sequence #183.
DE

XX PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
XX dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
XX blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
XX adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
XX
XX Homo sapiens.
XX
XX WO200168848-A2.
XX
XX 20-SEP-2001.
XX
XX 28-FEB-2001; 2001WO-US006520.
XX
XX 01-MAR-2000; 2000MO-US005601.
XX 02-MAR-2000; 2000MO-US005841.
XX 03-MAR-2000; 2000US-0187202P.
XX 06-MAR-2000; 2000US-0186968P.
XX 14-MAR-2000; 2000US-0189320P.
XX 14-MAR-2000; 2000US-0189328P.
XX 15-MAR-2000; 2000MO-US006884.
XX 21-MAR-2000; 2000US-0190828P.
XX 21-MAR-2000; 2000US-0191007P.
XX 21-MAR-2000; 2000US-0191048P.
XX 21-MAR-2000; 2000US-0191314P.
XX 28-MAR-2000; 2000US-0192655P.
XX 28-MAR-2000; 2000US-0193032P.
XX 29-MAR-2000; 2000US-0193033P.
XX 30-MAR-2000; 2000MO-US008439.
XX 04-APR-2000; 2000US-0194449P.
XX 04-APR-2000; 2000US-0194647P.
XX 11-APR-2000; 2000US-0195975P.
XX 11-APR-2000; 2000US-0196000P.
XX 11-APR-2000; 2000US-0196187P.
XX 11-APR-2000; 2000US-0196820P.
XX 11-APR-2000; 2000US-0196820P.
XX 18-APR-2000; 2000US-0198121P.
XX 18-APR-2000; 2000US-0198585P.
XX 25-APR-2000; 2000US-0199397P.
XX 25-APR-2000; 2000US-0199550P.
XX 25-APR-2000; 2000US-0199654P.
XX 03-MAY-2000; 2000US-0201516P.
XX 17-MAY-2000; 2000MO-US013705.
XX 22-MAY-2000; 2000MO-US014042.
XX 30-MAY-2000; 2000MO-US014941.
XX 02-JUN-2000; 2000MO-US015264.
XX 05-JUN-2000; 2000US-0209832P.
XX 28-JUL-2000; 2000MO-US020710.
XX 22-AUG-2000; 2000US-00644848.
XX 24-AUG-2000; 2000MO-US023328.
XX 08-NOV-2000; 2000MO-US030952.
XX 01-DEC-2000; 2000MO-US032678.
XX 20-DEC-2000; 2000MO-US034956.
XX
XX (GETH) GENENTECH INC.
XX
XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL,
XX Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z,
XX
XX WPI; 2001-602746/68.
XX N-PSDB; AAS46107.
XX
XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the
XX PT presence of tumors, such as prostate and breast tumors, in mammals and to
XX PT screen for modulators of the compounds.
XX
XX Claim 11; Fig 366; 774bp; English.
XX
XX Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
XX CC The PRO polypeptides and their associated nucleic acids can be used to
XX CC detect the presence of a tumour in a mammal by comparing the level of
XX CC expression of a PRO polypeptide in a test sample of cells from the animal
XX CC and a control sample of normal cells, whereby a higher level of


```

XX 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0064215P.
PR 22-APR-1998; 98US-0082797P.
PR 25-APR-1998; 98US-0083495P.
PR 15-MAY-1998; 98US-0085579P.
PR 02-JUN-1998; 98US-0087759P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088030P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088740P.
PR 10-JUN-1998; 98US-0088811P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088825P.
PR 11-JUN-1998; 98US-0088863P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089653P.
PR 19-JUN-1998; 98US-0089952P.
PR 22-JUN-1998; 98US-0090246P.
PR 24-JUN-1998; 98US-0090444P.
PR 25-JUN-1998; 98US-0090688P.
PR 25-JUN-1998; 98US-0090696P.
PR 26-JUN-1998; 98US-0090862P.
PR 02-JUL-1998; 98US-0091628P.
PR 10-AUG-1998; 98US-0096012P.
PR 17-AUG-1998; 98US-0096757P.
PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096959P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097979P.
PR 01-SEP-1998; 98US-0098749P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099792P.
PR 10-SEP-1998; 98US-0099812P.
PR 10-SEP-1998; 98US-0099815P.
PR 16-SEP-1998; 98US-0100627P.
PR 16-SEP-1998; 98US-0100629P.
PR 16-SEP-1998; 98US-0100630P.
PR 17-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100930P.
PR 22-SEP-1998; 98US-0101279P.
PR 23-SEP-1998; 98US-0101475P.
PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101743P.
PR 24-SEP-1998; 98US-0101916P.
PR 30-SEP-1998; 98US-0102570P.
PR 06-OCT-1998; 98US-0103449P.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021194.
PR 22-DEC-1999; 99WO-US030720.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 01-MAR-2000; 2000WO-US005601.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 10-NOV-2000; 2000WO-US030873.
PR 10-DEC-2000; 2000WO-US032378.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.

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PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
XX
XX (GENTH ) GENENTECH INC.
PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WJ;
XX
XX MPI; 2002-731348/79.
DR N-PSDB; ABS74438.
XX
PT New isolated secreted and transmembrane PRO polypeptide useful for
PT modulating biological activity of a cell, or for treating sports-related
PT joint problems, osteoarthritis or rheumatoid arthritis.
XX
XX Claim 20; Fig 122; 399p; English.
XX
CC The invention relates to an isolated secreted and transmembrane PRO
CC polypeptide having 80 % sequence identity to a sequence appearing as
CC ABG55851-ABG55934 or their associated signal peptide, or a sequence of an
CC extracellular domain of the proteins with their associated signal peptide
CC or lacking its associated signal peptide. Also included are the nucleic
CC acids encoding the proteins, vectors, host cells, fusion proteins and
CC antibodies which specifically bind to the proteins. The proteins are
CC useful for detecting a polypeptide designated as A, B, C or D in a sample
CC suspected of containing an A, B, C or D polypeptide, by contacting the
CC sample with a polypeptide designated as E, F, G, H or I (or vice versa)
CC and determining the formation of a A/E, B/F, G/G, C/H or D/I polypeptide
CC conjugate in the sample, where the formation of the conjugate is
CC indicative of the presence of an A, B, C or D polypeptide in the sample,
CC where A is a PRO10272 polypeptide, B is a PRO20110 polypeptide, C is a
CC PRO10096 polypeptide, D is a PRO19760 polypeptide, E is a PRO5801
CC polypeptide, F is a PRO1 polypeptide, G is a PRO20040 polypeptide, H is a
CC PRO20233 polypeptide and I is a PRO1890 polypeptide. The sample comprises
CC a cell suspected of expressing the A, B, C or D polypeptide. The B, F, G,
CC H or I polypeptide is labeled with a detectable label or is attached to a
CC solid support. The proteins are useful for linking a bioactive molecule
CC to a cell expressing a polypeptide designated as A, B, C or D or E, F, G,
CC H or I. The bioactive molecule is a toxin, a radiolabel or an antibody.
CC The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H,
CC or I, or antibodies against them are useful for modulating a biological
CC activity of a cell expressing a polypeptide designated as A, B, C or D or
CC E, F, G, H, or I. The cell is killed. The proteins are useful for
CC identifying agonists or antagonists, for the preparation of a medicament
CC useful in the treatment of a condition which is responsive to the
CC proteins, as molecular weight markers for protein electrophoresis
CC purposes, and as therapeutic agents for treating sports-related joint
CC problems, articular cartilage defects, osteoarthritis or rheumatoid
CC arthritis. Nucleic acids encoding the proteins are useful as
CC hybridisation probes, in chromosome and gene mapping, in the generation
CC of anti-sense RNA and DNA, for the preparation of the proteins, to
CC generate transgenic or knockout animals which are useful in the
CC development and screening of therapeutic useful reagents, for chromosome
CC identification, and in gene therapy. The antibody is useful as a
CC therapeutic agent, in a diagnostic assay and for affinity purification of
CC the protein from recombinant cell culture natural sources. The present
CC invention represents a novel secreted or transmembrane protein of the
CC
XX
SQ Sequence 243 AA;
Query Match 100.0%; Score 1301; DB 5; Length 243;
Best Local Similarity 100.0%; Pred. No. 3,25-121;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRPQGPASPORTLRGLILLILLQLPAPSSASITPRKQKAKQKRGVVDLYNKMCLQGA 60
DB 1 MRPQGPASPORTLRGLILLILLQLPAPSSASITPRKQKAKQKRGVVDLYNKMCLQGA 60
QY 61 GVPRDGSFGANVIVDTGPIPRDGFKEBKECLRESFEESWTPTYKQCSWSLNYGIDL 120

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Db 61 GVGGRDSSPGANVITPGTGPGRDGFGEKGECLRESFESWTPNVKQCSMSLNYGIDL 120
 QY 121 GKIAECTFTKRSNSALRVLFSGSLKCKNACCGWYTFNCAEGSGPLPIEAIYYDQ 180
 Db 121 GKIAECTFTKRSNSALRVLFSGSLKCKNACCGWYTFNCAEGSGPLPIEAIYYDQ 180
 QY 181 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIIVGTCSDDYPRGDASTGMSVSRITIEE 240
 Db 181 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIIVGTCSDDYPRGDASTGMSVSRITIEE 240
 QY 241 LPK 243
 Db 241 LPK 243

RESULT 8
 ID ABB84939 standard; protein; 243 AA.
 AC ABB84939;

DT 16-MAY-2002 (first entry)
 DE Human PRO1550 protein sequence SEQ ID NO:246.
 XX

KW Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;
 KW vunerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
 KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;
 KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
 KW age-related macular degeneration; arterial restenosis; angina;
 KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;
 KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
 KW wound healing; chromosome mapping; gene mapping.

OS Homo sapiens.

PN WC0200200690-A2.

XX 03-JAN-2002.

PF 20-JUN-2001; 2001WO-US019692.

XX 23-JUN-2000; 2000US-0213637P.
 PR 20-JUL-2000; 2000US-0219556P.
 PR 25-JUL-2000; 2000US-0220624P.
 PR 28-JUL-2000; 2000US-0220644P.
 PR 02-AUG-2000; 2000US-0220710P.
 PR 17-AUG-2000; 2000US-0226959P.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 07-SEP-2000; 2000US-0230978P.
 PR 18-SEP-2000; 2000US-00664610.
 PR 18-SEP-2000; 2000US-00665350.
 PR 24-OCT-2000; 2000US-0249222P.
 PR 08-NOV-2000; 2000US-00709238.
 PR 08-NOV-2000; 2000WO-US019692.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 22-JAN-2001; 2001US-00767609.
 PR 28-FEB-2001; 2001US-00796498.
 PR 01-MAR-2001; 2001WO-US0066520.
 PR 09-MAR-2001; 2001US-00806666.
 PR 14-MAR-2001; 2001US-00802706.
 PR 22-MAR-2001; 2001US-00808689.
 PR 05-APR-2001; 2001US-00816744.
 PR 10-MAY-2001; 2001US-00828366.
 PR 10-MAY-2001; 2001US-00854280.
 PR 25-MAY-2001; 2001US-00866028.

PR 25-MAY-2001; 2001US-00866034.
 PR 25-MAY-2001; 2001WO-US017092.
 PR 30-MAY-2001; 2001US-00870574.
 PR 30-MAY-2001; 2001WO-US017443.
 PR 01-JUN-2001; 2001WO-US017800.

FA (BETH) GENENTECH INC.

PI Baker KP, Ferrara N, Garber H, Gerritsen ME, Goddard A,
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF,
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W,
 XX NPI, 2002-090516/12.
 DR N-PSDB; ABL88194.

XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 PT infarction), endothelial or angiogenic disorders in a mammal.

PS Claim 11, Fig 246; 565pp; English.

XX ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
 CC ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,
 CC antiangiogenic, hypotensive, vunerary and antiarteriosclerotic
 CC activities, and can be used in gene therapy. The PRO polynucleotides,
 CC proteins, agonists and antagonists are useful for treating or diagnosing
 CC cardiac hypertrophy, trauma, cancer, age-related macular degeneration,
 CC angina, myocardial infarction, arterial restenosis, rheumatoid arthritis,
 CC lymphangitis, tumour angiogenesis and liver carcinoma) and wound
 CC healing. The PRO polynucleotides have applications in molecular biology,
 CC including use as hybridisation probes, and in chromosome and gene
 CC mapping. ABB88259 to ABL88267 represent primers and probes used in the
 CC exemplification of the present invention

XX Sequence 243 AA;

Query Match 100.0%; Score 1301; DB 5; Length 243;
 Best Local Similarity 100.0%; Pred. No. 3.2e-121;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPGSPAASPORLRLGLLLQLLPAPASASEIPKQKQKQRLRREYVDLYNMCQOGPA 60
 Db 1 MRPGSPAASPORLRLGLLLQLLPAPASASEIPKQKQKQRLRREYVDLYNMCQOGPA 60
 QY 61 GVGGRDSSPGANVITPGTGPGRDGFGEKGECLRESFESWTPNVKQCSMSLNYGIDL 120
 Db 61 GVGGRDSSPGANVITPGTGPGRDGFGEKGECLRESFESWTPNVKQCSMSLNYGIDL 120
 QY 121 GKIAECTFTKRSNSALRVLFSGSLRCKRNACCGWYTFNCAEGSGPLPIEAIYYDQ 180
 Db 121 GKIAECTFTKRSNSALRVLFSGSLRCKRNACCGWYTFNCAEGSGPLPIEAIYYDQ 180
 QY 181 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIIVGTCSDDYPRGDASTGMSVSRITIEE 240
 Db 181 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIIVGTCSDDYPRGDASTGMSVSRITIEE 240
 QY 241 LPK 243
 Db 241 LPK 243

RESULT 9
 ID AAE20462 standard; protein; 243 AA.
 AC AAE20462;

DT 01-JUL-2002 (first entry)

DE Human tumour-associated antigenic target-170 (TA1170) protein.

01-JUN-2001; 2001WO-US017800.
20-JUN-2001; 2001WO-US019692.

(GERTH) GENENTECH INC.
(BAKER) BAKER K P.
(FERR) FERRARA N.
(GERB) GERBER H.
(GERR) GERRITSEN M E.
(GODD) GODDARD A.
(GODD) GODDARD P J.
(GURNE) GURNEY A L.
(HILL) HILLAN K J.
(MARS) MARSTERS S A.
(PANU) PAN J.
(PAON) PAONI N F.
(STEP) STEPHAN J F.
(WATA) WATANABE C K.
(WILL) WILLIAMS P M.
(WOOD) WOOD W I.

Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF, Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W, Paoni NF, WPI; 2002-171999/22.
N-PSDB; ABL95683.

One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal.
Claim 11; Fig 246; 567DP; English.

The present invention provides the protein and coding sequences of human PRO proteins. These are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder, including cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial stenosis, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The present sequence is a PRO protein of the invention

Sequence 243 AA;

Query Match 100.0%; Score 1301; DB 5; Length 243;
Best Local Similarity 100.0%; Pred. No. 3, 2e-121;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MRPGPASPQRLKGLLLILLQLPAPSSASEIPKQKQKQRLQREVVLDVNGMCLQGPA 60
1 MRPGPASPQRLKGLLLILLQLPAPSSASEIPKQKQKQRLQREVVLDVNGMCLQGPA 60
61 GVPGRDGSFGANVIGTPGIPGRDGFKEGKEGECLESPFESWTPTYKQCSMSLNYGIDL 120
61 GVPGRDGSFGANVIGTPGIPGRDGFKEGKEGECLESPFESWTPTYKQCSMSLNYGIDL 120
121 GKIACTTTKRSNSALRVLFSGSLRLKCRNACCQRMWFTFNGACSGPLPIEAIITYDQ 180
121 GKIACTTTKRSNSALRVLFSGSLRLKCRNACCQRMWFTFNGACSGPLPIEAIITYDQ 180
121 GKIACTTTKRSNSALRVLFSGSLRLKCRNACCQRMWFTFNGACSGPLPIEAIITYDQ 180
181 GSPENNSTINIRTSVSGCEGIGAGLVDAIWTGTSYTPKGDASTGMSVSRITIEE 240
181 GSPENNSTINIRTSVSGCEGIGAGLVDAIWTGTSYTPKGDASTGMSVSRITIEE 240
241 LPK 243
241 LPK 243

RESULT 11
ABP68636
ID ABP68636 standard; protein; 243 AA.

AC ABP68636;
DT 14-JAN-2003 (first entry)
DE Human pancreatic cancer expressed protein SEQ ID NO 4559.
KW Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;
KM cytostatic; tumour.
OS Homo sapiens.
PN WO200260317-A2.
PD 08-AUG-2002.
PF 30-JAN-2002; 2002WO-US002781.
PR 30-JAN-2001; 2001US-0265305P.
PR 31-JAN-2001; 2001US-0265682P.
PR 09-FEB-2001; 2001US-0267568P.
PR 21-MAR-2001; 2001US-0278651P.
PR 28-APR-2001; 2001US-0287112P.
PR 16-MAY-2001; 2001US-0291631P.
PR 12-JUL-2001; 2001US-0305484P.
PR 20-AUG-2001; 2001US-0313999P.
PR 27-NOV-2001; 2001US-0333626P.

(CORI-) CORIYA CORP.
Benson DR, Kalos MD, Lodes MJ, Persing DH, Hepler WT, Jiang Y, WPI; 2002-627435/67.
N-PSDB; ABV99144.

New isolated polynucleotide and pancreatic tumor polypeptides, useful for diagnosing, preventing and/or treating cancer, particularly pancreatic cancer.

Claim 2; SEQ ID NO 4559; 300bp + Sequence Listing; English.

The invention relates to an isolated polynucleotide (1) comprising: (a) any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b) complements of (a); (c) sequences consisting of at least 20 contiguous residues of (a); (d) sequences that hybridize to (a) under moderately stringent conditions; (e) sequences having at least 75% or 90% identity to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596-ABP68637) encoded by (1) and oligonucleotide can be used to detect cancer in a patient and compositions comprising polypeptides, polynucleotides, antibodies, fusion proteins, T cell populations and antigen presenting cells expressing the polypeptide are useful in treating pancreatic cancer and stimulating an immune response. The polynucleotides can be used as probes or primers for nucleic acid hybridization, in the design and preparation of ribozyme molecules for inhibiting expression of the tumour polypeptides and proteins in the tumour cells, in vaccines and for gene therapy. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at http://wipo.int/pub/published_pct_sequences

Query Match 100.0%; Score 1301; DB 5; Length 243;
Best Local Similarity 100.0%; Pred. No. 3, 2e-121;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MRPGPASPQRLKGLLLILLQLPAPSSASEIPKQKQKQRLQREVVLDVNGMCLQGPA 60
1 MRPGPASPQRLKGLLLILLQLPAPSSASEIPKQKQKQRLQREVVLDVNGMCLQGPA 60
61 GVPGRDGSFGANVIGTPGIPGRDGFKEGKEGECLESPFESWTPTYKQCSMSLNYGIDL 120
61 GVPGRDGSFGANVIGTPGIPGRDGFKEGKEGECLESPFESWTPTYKQCSMSLNYGIDL 120
121 GKIACTTTKRSNSALRVLFSGSLRLKCRNACCQRMWFTFNGACSGPLPIEAIITYDQ 180

Db 121 GKIAECTFTKMSNSALRVLFSGSLRLKCRNACCQWYFTFNCAEGSGPLPIEAIYYLDQ 180
Qy 181 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIWMGTCSDPYKGDASTGMNSVSRIIIE 240
Db 181 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIWMGTCSDPYKGDASTGMNSVSRIIIE 240
Qy 241 LPK 243
Db 241 LPK 243
RESULT 12
ABG78938
ID ABG78938 standard; protein; 243 AA.
AC ABG78938;
XX 15-NOV-2002 (first entry)
DT 15-NOV-2002 (first entry)
XX
DE Human breast tumour polypeptide #29.
XX
KW Human; breast tumour protein; breast cancer; cytostatic; vaccine.
XX
OS Homo sapiens.
XX
PN US2002085998-A1.
XX
PD 04-JUL-2002.
XX
PF 13-APR-2001; 2001US-00834759.
XX
PR 28-DEC-1998; 98US-00223575.
PR 02-APR-1999; 99US-00285480.
PR 23-JUN-1999; 99US-00339338.
PR 02-SEP-1999; 99US-00389681.
PR 03-NOV-1999; 99US-00433826.
PR 17-APR-2000; 2000US-00551621.
PR 08-JUN-2000; 2000US-00590751.
PR 22-JUN-2000; 2000US-00604287.
PR 20-JUL-2000; 2000US-00620405.
XX
XX
PA (CORI-) CORIXA CORP.
XX
PI Jiang Y, Dillon DC, Mitcham JL, Xu J, Harlocker SL, Hepler WT;
PI Henderson RA;
XX
XX MPI; 2002-635657/68.
DR N-PSDB; AB64028, AB64029.
XX
XX Novel breast cancer polynucleotides and polypeptides encoded by the
PT polynucleotides, useful for detecting the presence of breast cancer in a
PT patient, and in pharmaceutical compositions, for treating breast cancer.
XX
XX Claim 2; Page 235-236; 247pp; English.
XX
XX The invention relates to an isolated breast tumour polynucleotide and the
CC polypeptide it encodes. The polynucleotide and polypeptide are useful for
CC detecting the presence of breast cancer in a patient, and in
CC pharmaceutical compositions for treating breast cancer. The sequences are
CC useful for stimulating an immune response in a patient and can therefore
CC be used in production of vaccines. The sequences are also useful for
CC detecting the presence of a cancer in a patient, by obtaining a
CC biological sample from the patient, contacting the biological sample with
CC a composition of the invention and detecting the amount of polynucleotide
CC that hybridizes to the sample. This sequence represents a human breast
CC tumour polypeptide of the invention
XX
XX Sequence 243 AA;
SQ

Qy 1 MRPOGPASPORLRLGLLLILLQLPAPSSASEIPKQKAKOLROREVVDLYNMGCLQGA 60
Db 1 MRPOGPASPORLRLGLLLILLQLPAPSSASEIPKQKAKOLROREVVDLYNMGCLQGA 60
Qy 61 GVPGRDGPANVIRPOTPGIPGRDPFKGEKGECLRESFEESWTIPNYKQCSWLSNYGIDL 120
Db 61 GVPGRDGPANVIRPOTPGIPGRDPFKGEKGECLRESFEESWTIPNYKQCSWLSNYGIDL 120
Qy 121 GKIAECTFTKMSNSALRVLFSGSLRLKCRNACCQWYFTFNCAEGSGPLPIEAIYYLDQ 180
Db 121 GKIAECTFTKMSNSALRVLFSGSLRLKCRNACCQWYFTFNCAEGSGPLPIEAIYYLDQ 180
Qy 181 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIWMGTCSDPYKGDASTGMNSVSRIIIE 240
Db 181 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIWMGTCSDPYKGDASTGMNSVSRIIIE 240
Qy 241 LPK 243
Db 241 LPK 243
RESULT 13
ABUS8582
ID ABUS8582 standard; protein; 243 AA.
AC ABUS8582;
XX
XX 15-APR-2003 (first entry)
DT 15-APR-2003 (first entry)
XX
DE Human PRO polypeptide #183.
XX
KW Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;
KW dog; cat; cow; horse; sheep; pig; goat; rabbit; ADPFT;
KW antibody-dependent enzyme mediated prodrug therapy.
XX
OS Homo sapiens.
XX
PN US2003027272-A1.
XX
PD 06-FEB-2003.
XX
PF 21-JUN-2002; 2002US-00176492.
XX
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 17-OCT-1997; 97US-0062450P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063540P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063734P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066120P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066722P.
PR 11-DEC-1997; 97US-0069335P.
PR 12-DEC-1997; 97US-0069425P.
PR 17-DEC-1997; 97US-0069870P.
PR 18-DEC-1997; 97US-0068017P.
PR 10-MAR-1998; 98US-0074507P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077649P.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078839P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079786P.
PR 31-MAR-1998; 98US-0080107P.

PR 31-MAR-1998; 98US-0080194P.
PR 01-APR-1998; 98US-0080327P.
PR 01-APR-1998; 98US-0080333P.
PR 08-APR-1998; 98US-0081049P.
PR 08-APR-1998; 98US-0081070P.
PR 09-APR-1998; 98US-0081195P.
PR 15-APR-1998; 98US-0081838P.
PR 21-APR-1998; 98US-0082568P.
PR 21-APR-1998; 98US-0082569P.
PR 22-APR-1998; 98US-0082704P.
PR 22-APR-1998; 98US-0083322P.
PR 28-APR-1998; 98US-0083495P.
PR 29-APR-1998; 98US-0083496P.
PR 29-APR-1998; 98US-0083499P.
PR 29-APR-1998; 98US-0083559P.
PR 29-APR-1998; 98US-0083566P.
PR 06-MAY-1998; 98US-0084414P.
PR 07-MAY-1998; 98US-0084639P.
PR 07-MAY-1998; 98US-0084640P.
PR 15-MAY-1998; 98US-0084643P.
PR 15-MAY-1998; 98US-0085580P.
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QY 61 GVPGGDGSAGAVIPCTPGIPGRDGFKGKGCILRSEFESMTPNKQCSWSLNYGIDL 120
DB 61 GVPGGDGSAGAVIPCTPGIPGRDGFKGKGCILRSEFESMTPNKQCSWSLNYGIDL 120
QY 121 GRIACCTFKRMSNSALRYLFGSLRLKCRNACCORWYTFNGAECGSLPIEATIIYLDQ 180
DB 121 GRIACCTFKRMSNSALRYLFGSLRLKCRNACCORWYTFNGAECGSLPIEATIIYLDQ 180
QY 181 GSPENNSTINIHRTSSVEGLCEGIGAGLYDVAIWGTCSDYDPKGDASTGMSVSRIIIEE 240
DB 181 GSPENNSTINIHRTSSVEGLCEGIGAGLYDVAIWGTCSDYDPKGDASTGMSVSRIIIEE 240
QY 241 LPK 243
DB 241 LPK 243

RESULT 14

ABU88130
ID ABU88130 standard; protein; 243 AA.

XX ABU88130;

DT 07-JUL-2003 (first entry)

DE Novel human secreted and transmembrane protein PRO1550.

XX Human; secreted and transmembrane protein; PRO; gene therapy;
KW tumour necrosis factor-alpha release; TNF-alpha release;
KW chondrocyte proliferation; chondrocyte differentiation; tumour;
KW adrenal tumour; lung tumour; colon tumour; breast tumour;
KW prostate tumour; rectal tumour; cervical tumour; liver tumour.

XX Homo sapiens.

PN US2003032127-A1.

PD 13-FEB-2003.

PF 26-JUN-2002; 2002US-00183012.

XX 18-SEP-1997; 97US-0059263P.
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Dd	1 MRPOPPAASPORLIGLLILLILLOLPAPSSASEIPKGGOKALRRREVDLYNMCLOGPA	60				
Qy	61 GVPGGDGGPGANNVPCGPGIPEGDDCKKGKEGCLRESFEESWTPNNYKQCSWSLVNYGIDL	120				
Dd	61 GVPGGDGGPGANNVPCGPGIPEGDDCKKGKEGCLRESFEESWTPNNYKQCSWSLVNYGIDL	120				
Qy	121 GKIAECTPYTKRNSALRYLVFGSLRLKCRNAACORWFTFPNGAECSGLPEATIIYLDO	180				
Dd	121 GKIAECTPYTKRNSALRYLVFGSLRLKCRNAACORWFTFPNGAECSGLPEATIIYLDO	180				
Qy	181 GSPEWNTINIHRTSSVEGLCEGICAGLYDVAVLWGTCSDYPKGDASTGMNSVSRIIEE	240				
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ID	ABU84445 standard; protein; 243 AA.					
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DT	02-AUG-2003 (first entry)					
DE	Human secreted/transmembrane protein (PRO) #183.					
KM	Human; secreted and transmembrane protein; PRO; TNF-alpha;					
KW	tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;					
RW	tissue typing.					
OS	Homo sapiens.					
PN	US2003032112-A1.					
PD	13-FEB-2003.					
PF	21-JUN-2002; 2002US-00176756.					
PR	18-SEP-1997; 97US-0059263P.					
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PR 18-SEP-1998; 98US-0101014P.

PR 18-SEP-1998; 98US-0101068P.
PR 23-SEP-1998; 98US-0101471P.
PR 23-SEP-1998; 98US-0101472P.
PR 23-SEP-1998; 98US-0101475P.
PR 23-SEP-1998; 98US-0101477P.
PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101739P.
PR 24-SEP-1998; 98US-0101743P.
PR 25-SEP-1998; 98US-0101922P.
PR 25-SEP-1998; 98US-0101786P.
PR 29-SEP-1998; 98US-0102240P.
PR 29-SEP-1998; 98US-0102240P.
PR 29-SEP-1998; 98US-0102331P.
PR 30-SEP-1998; 98US-0102331P.
PR 30-SEP-1998; 98US-0102487P.
PR 30-SEP-1998; 98US-0102571P.
PR 01-OCT-1998; 98US-0102684P.
PR 01-OCT-1998; 98US-0102687P.
PR 02-OCT-1998; 98US-0102965P.
PR 06-OCT-1998; 98US-0103258P.
PR 07-OCT-1998; 98US-0103449P.
PR 07-OCT-1998; 98US-00168978.

Query Match 100.0%; Score 1301; DB 6; Length 243;
Best Local Similarity 100.0%; Pred. No. 3.2e-121; Indels 0; Gaps 0;
Matches 243; Conservative 0; Mismatches 0;

QY 1 MRPGPASPQRRLGLLILLLQLPAPSSASEIPKQKQALRQREVDLYNGMCLQGPA 60
DB 1 MRPGPASPQRRLGLLILLLQLPAPSSASEIPKQKQALRQREVDLYNGMCLQGPA 60
QY 61 GVPGRDGSFGANYIPGTGIPGRDGFKEGKECLRESFESWTPTNYKQCSWSLNYGIDL 120
DB 61 GVPGRDGSFGANYIPGTGIPGRDGFKEGKECLRESFESWTPTNYKQCSWSLNYGIDL 120
QY 121 GKIAECTFTKMRNSALRYLFSGLRLKCRNACCQRMWFTFNGAECGPIEATIIYLDQ 180
DB 121 GKIAECTFTKMRNSALRYLFSGLRLKCRNACCQRMWFTFNGAECGPIEATIIYLDQ 180
QY 181 GSPENNSTINIHRTSVBGLCEGIGAGLYDVVAIWGTCSDYPRGDASTGMNSVSRITIEE 240
DB 181 GSPENNSTINIHRTSVBGLCEGIGAGLYDVVAIWGTCSDYPRGDASTGMNSVSRITIEE 240
QY 241 LFK 243
DB 241 LFK 243

Search completed: December 25, 2004, 05:25:48
Job time : 80 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 25, 2004, 05:09:56 ; Search time 96 Seconds
(without alignments)
1456.417 Million cell updates/sec

Title: US-10-063-734-122

Perfect score: 1301

Sequence: 1 MRPGPAASPORTRLGILLLL.....GPASTGWSVSRRIIEELPK 243

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: UniProt 02.*

1: uniprot_prot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1301	100.0	243	2	Q6UW91
2	1301	100.0	243	2	AAG89273
3	1294	99.5	243	2	Q96C68
4	1266	93.5	245	2	Q8CG08
5	1201	92.3	245	2	Q9D1D6
6	1052	80.9	232	2	Q81X63
7	132	10.1	565	2	Q8K036
8	124.5	9.6	717	2	Q9NQ52
9	122.5	9.4	246	1	C1OC_MOUSE
10	122.5	9.4	1472	2	Q9Q2A0
11	120	9.2	287	2	Q8CFR0
12	120	9.2	1752	2	Q07265
13	119	9.1	289	2	Q18799
14	118.5	9.1	358	2	Q6MEY7
15	118.5	9.1	358	2	CAF22862
16	118.5	9.1	1069	2	Q6LAN8
17	118.5	9.1	1069	2	CA67261
18	118.5	9.1	1461	1	Q76045
19	118.5	9.1	1464	1	CA11_HUMAN
20	118.5	9.1	1464	2	Q8NA73
21	118	9.1	291	2	Q9NAR3
22	118	9.1	832	2	Q96F77
23	118	9.1	1860	2	Q812C6
24	117.5	9.0	540	2	Q86Y22
25	117.5	9.0	568	2	Q8CD80
26	117.5	9.0	739	2	Q70575
27	117.5	9.0	747	2	Q6NWS7
28	117.5	9.0	747	2	AA67716
29	117.5	9.0	751	2	Q9RIN9
30	117	9.0	327	2	Q01799
31	117	9.0	754	1	CA54_CANFA

32	117	9.0	1447	2	Q6PAU1
33	117	9.0	1447	2	Q6U1J5
34	117	9.0	1447	2	AA63249
35	117	9.0	1447	2	AA24536
36	117	9.0	1669	2	Q9Q2S0
37	116	8.9	551	2	Q6ZM13
38	116	8.9	551	2	BAD18742
39	116	8.9	886	2	Q9NUR7
40	116	8.9	888	2	Q90796
41	116	8.9	1670	1	CA34_HUMAN
42	116	8.9	1685	1	CA54_HUMAN
43	115.5	8.9	289	1	Q077_HUMAN
44	115.5	8.9	1075	2	Q86X41
45	115.5	8.9	1336	2	Q6RZ41

ALIGNMENTS

RESULT 1

ID	Q6UW91	PRELIMINARY;	PRT;	243 AA.
AC	Q6UW91			
DT	05-JUL-2004	(TREMBLrel. 27, Created)		
DT	05-JUL-2004	(TREMBLrel. 27, Last sequence update)		
DT	05-JUL-2004	(TREMBLrel. 27, Last annotation update)		
DE	CTHRC1			
GN	ORFName=UNQ762;			
OS	Homio sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
OX	NCBI_Taxid=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=22887296; PubMed=12975309;			
RA	Clark H.F., Gurney A.L., Adaya E., Baker K., Baldwin D., Brush J.,			
RA	Chen J., Chow B., Chui C., Crowley C., Currell B., Devel B., Dowd P.,			
RA	Huang A., Foster J., Grimaldi C., Gu Q., Haas P.E., Haldens S.,			
RA	Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,			
RA	Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,			
RA	Vandlen R., Watanabe C., Wleand D., Woods K., Xie M.H., Yansura D.,			
RA	Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,			
RA	Godowski P.			
RT	"The secreted protein discovery initiative (SPDI), a large-scale			
RT	effort to identify novel human secreted and transmembrane proteins: a			
RT	bioinformatics assessment."			
RL	Genome Res. 13:2265-2270(2003).			
DR	EMBL; AY358914; AAQ89273.1; -			
DR	InterPro; IPR008161; Clg_helix.			
DR	InterPro; IPR008160; Collagen.			
DR	Prodom; PD000007; Clg_helix; 1.			
KW	COLLAGEN.			
SC	SEQUENCE 243 AA; 26266 MW; BCB49AF4DBC303BC CRC64;			

Query Match 100.0%; Score 1301; DB 2; Length 243;
Best Local Similarity 100.0%; Pred. No. 6.5e-108; Mismatches 0; Indels 0; Gaps 0;

QY	1	MRPGPAASPORTRLGILLLLQLPAPSASERIPKQKQAQLREBVDLYNGMCLOGPA	60
DB	1	MRPGPAASPORTRLGILLLLQLPAPSASERIPKQKQAQLREBVDLYNGMCLOGPA	60
QY	61	GVPRGDSFGANVIGTFCIGIPGRDPFKGKGCLEBSEFTPYKQCSWSLNYGIDL	120
DB	61	GVPRGDSFGANVIGTFCIGIPGRDPFKGKGCLEBSEFTPYKQCSWSLNYGIDL	120
QY	121	GKIARCTFTKMSNALTALVTFSGSLRLKCRNACQQRWTFPGARCSGLPTEATIIYLDQ	180
DB	121	GKIARCTFTKMSNALTALVTFSGSLRLKCRNACQQRWTFPGARCSGLPTEATIIYLDQ	180
QY	181	GSPENNSTINIRTSVEGLCEGIGAGLVDAIWIWGCSDPYKQSGASTGWSVSRRIIEE	240
DB	181	GSPENNSTINIRTSVEGLCEGIGAGLVDAIWIWGCSDPYKQSGASTGWSVSRRIIEE	240

DB 241 LPK 243

RESULT 4

Q8CG08 PRELIMINARY; PRT; 245 AA.

AC Q8CG08; 01-MAR-2003 (TREMBLrel. 23, last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, last sequence update)

DE 01-OCT-2003 (TREMBLrel. 25, last annotation update)

GN Name=Chrc1;

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

NCBI_TaxID=10116;

SEQUENCE FROM N.A.

RA STRAIN=Sprague-Dawley; TISSUE=8 day balloon-injured carotid artery; Lehnert W., Moore D.P., Harmon K.J., Mancini M.L., Lindner V.; Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.

RL EMBL; AY136824; AAN15748.1; -

DR GO; GO:0005737; C:cytoplasm; IEA.

DR GO; GO:0006817; P:phosphate transport; IEA.

DR InterPro; IPR008161; Clg helix.

DR InterPro; IPR008160; Collagen.

DR Pfam; PF01391; Collagen.1.

DR Prodom; PD000007; Clg_helix; 1.

KW Collagen.

SEQUENCE 245 AA; 26424 MW; 2296FD6DCDBA21F2 CRC64;

Query Match 93.5%; Score 1216; DB 2; Length 245;

Best Local Similarity 94.3%; Pred. No. 2,6e-100; Matches 231; Conservative 3; Mismatches 9; Indels 2; Gaps 1;

QY 1 MRPGPAASPPRLRG-LTLTLTLTLQAPSSASEIPKQKQQLRQREVDLYNQCLOG 58

DB 1 MHPGRASPOLLGFLVLLTLQLSASSASBNPKVQKLLINREVDLYNQCLOG 60

QY 59 PAVPGRDGGPGANVYIPGTPIGRDGFKEGKEGECRESFEESWTPNPKQCSWSSINYG 118

DB 61 PAVGVRDGGPGANVYIPGTPIGRDGFKEGKEGECRESFEESWTPNPKQCSWSSINYG 120

QY 119 DLGKIAECTFTMRNSALRVLPSSGLRCKRNACCQRYFTFNAGCGPPIEATLYL 178

DB 121 DLGKIAECTFTMRNSALRVLPSSGLRCKRNACCQRYFTFNAGCGPPIEATLYL 180

QY 179 DQSGEMNSTINIHRTSSVEGLCEGIGAGLVVAIVWTCSDYPKGDASTGNNSVSRIT 238

DB 181 DQSGEMNSTINIHRTSSVEGLCEGIGAGLVVAIVWTCSDYPKGDASTGNNSVSRIT 240

QY 239 EELPK 243

DB 241 EELPK 245

RESULT 5

Q9DID6 PRELIMINARY; PRT; 245 AA.

AC Q9DID6; 01-JUN-2001 (TREMBLrel. 17, last sequence update)

DT 01-JUN-2001 (TREMBLrel. 17, last sequence update)

DE 01-JUN-2003 (TREMBLrel. 24, last annotation update)

DE Mus musculus 18-day embryo whole body cDNA, RIKEN full-length enriched library, clone:110014807 product:hypothetical collagen triple helix repeat containing protein, full insert sequence.

GN Name=Chrc1;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;

SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=whole body; MEDLINE=99279253; PubMed=10349636;

RX Carninci P., Hayashizaki Y.; "High-efficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).

RL Nature 409:685-690(2001).

SEQUENCE FROM N.A.

RA STRAIN=C57BL/6J; TISSUE=whole body; MEDLINE=21085660; PubMed=11217851;

RX RIKEN FANTOM Consortium; "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).

SEQUENCE FROM N.A.

RA The FANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573(2002).

SEQUENCE FROM N.A.

RA STRAIN=C57BL/6J; TISSUE=whole body; MEDLINE=20499374; PubMed=11042159;

RX Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.; "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).

SEQUENCE FROM N.A.

RA STRAIN=C57BL/6J; TISSUE=whole body; MEDLINE=20530913; PubMed=11076861;

RX Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Kono H., Akiyama Y., Nishi K., Kitsuai T., Tashiro H., Itoh M., Sumi N., Iehi Y., Nakamura S., Hazama M., Nishine T., Kashiwagi K., Yamauchi R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujikawa S., Inoue K., Togawa Y., Izawa M., Ohara E., Wachihi M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai Y., Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.; "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer."; Genome Res. 10:1757-1771(2000).

SEQUENCE FROM N.A.

RA STRAIN=C57BL/6J; TISSUE=whole body; Aizawa K., Akahira S., Akimura T., Arai A., Aono H., Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M., Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F., Imotani K., Iehi Y., Itoh M., Izawa M., Kasukawa T., Kato H., Kawai J., Kojima Y., Kono H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numata R., Ohno M., Okazaki Y., Okido T., Owa C., Saito R., Sakai C., Sakai K., Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T., Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T., Tejima Y., Toyota T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M., Muramatsu M., Hayashizaki Y.; Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.

RA EMBL; AK003674; BAB22930.1; -

DR MGD; MGI:1915838; Chrc1.

DR GO; GO:0005737; C:cytoplasm; IEA.

DR GO; GO:0006817; P:phosphate transport; IEA.

DR InterPro; IPR008161; Clg helix.

DR InterPro; IPR008160; Collagen.

DR Pfam; PF01391; Collagen.1.

DR Prodom; PD000007; Clg_helix; 1.

KW Collagen; Hypothetical protein.

SEQUENCE 245 AA; 26460 MW; 14951B87D8181A0E CRC64;

Query Match 92.3%; Score 1201; DB 2; Length 245;

Best Local Similarity 93.1%; Pred. No. 5,6e-99; Matches 228; Conservative 4; Mismatches 11; Indels 2; Gaps 1;

QY 1 MRPGPASPORLRLG--LTLTLTLQLPAPSSASEIPKQKQAKLQREVVLDLYNMCLOG 58
 DB 1 MHPQGRAP.POLLGLFLVLLTLLOLSAPISASENPKYKQQLKQREVVLDLYNMCLOG 60
 QY 59 PAVPGRGSPGANVITPGTGGIPEGDFKGEKGECLRESFESWTPNYKQCSMSLNYGI 118
 DB 61 PAVPGRGSPGANVITPGTGGIPEGDFKGEKGECLRESFESWTPNYKQCSMSLNYGI 120
 QY 119 DLGRIACFTKMSNSALRYLFGSGILTKCRNACCQWYTFPNGAECGSLPTEAIYYL 178
 DB 121 DLGRIACFTKMSNSALRYLFGSGILTKCRNACCQWYTFPNGAECGSLPTEAIYYL 180
 QY 179 DQSPENASTINIHRTSSVEGLCEGIGAGLVDAIWTGTCSDYPRKGDASTGMSVSRIT 238
 DB 181 DQSPENASTINIHRTSSVEGLCEGIGAGLVDAIWTGTCSDYPRKGDASTGMSVSRIT 240
 QY 239 BELPK 243
 DB 241 BELPK 245

RESULT 6
 ID 081X63 PRELIMINARY; PRT; 232 AA.
 AC 081X63;
 DT 01-MAR-2003 (Tremblrel. 23, Created)
 DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE NTMCL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RA SEQUENCE FROM N.A.
 RA Sasaki N., Fujiki K., Kanai A., Tanaka Y., Iwata T.;
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AF395488; AA017919.1; -;
 DR GO; GO:0005737; C:cytoplasm; IEA.
 DR GO; GO:0006817; P:phosphate transport; IEA.
 DR InterPro; IPR008161; Clg_helix.
 DR InterPro; IPR008160; Collagen.
 DR Pfam; PF01391; Collagen; 1.
 DR Prodom; PD000007; Clg_helix; 1.
 KW Collagen.
 SQ SEQUENCE 232 AA; 25163 MW; E9D4BC30304837ED CRC64;

Query Match 80.9%; Score 1052; DB 2; Length 232;
 Best Local Similarity 83.1%; Pred. No. 1, le-85;
 Matches 201; Conservative 8; Mismatches 19; Indels 14; Gaps 2;
 QY 1 MRPGPASPORLRLG--LTLTLTLQLPAPSSASEIPKQKQAKLQREVVLDLYNMCLOGPA 60
 DB 1 MHPQGRAP.POLLGLFLVLLTLLOLSAPISASENPKYKQQLKQREVVLDLYNMCLOGPA 46
 QY 61 GVPGRDGSFGANVITPGTGGIPEGDFKGEKGECLRESFESWTPNYKQCSMSLNYGIDL 120
 DB 47 GVPGRDGSFGANVITPGTGGIPEGDFKGEKGECLRESFESWTPNYKQCSMSLNYGIDL 106
 QY 121 GRIACFTKMSNSALRYLFGSGILTKCRNACCQWYTFPNGAECGSLPTEAIYYL 180
 DB 107 GRIACFTKMSNSALRYLFGSGILTKCRNACCQWYTFPNGAECGSLPTEAIYYL 166
 QY 181 GSPENASTINIHRTSSVEGLCEGIGAGLVDAIWTGTCSDYPRKGDASTGMSVSRIT 240
 DB 167 GSPENASTINIHRTSSVEGLCEGIGAGLVDAIWTGTCSDYPRKGDASTGMSVSRIT 226
 QY 241 LP 242
 DB 227 LP 228

RESULT 7

Q8K036
 ID 08K036 PRELIMINARY; PRT; 565 AA.
 AC 08K036;
 DT 01-OCT-2002 (Tremblrel. 22, Created)
 DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
 DE Coll13a1 protein.
 GN Name=Coll13a1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RA SEQUENCE FROM N.A.
 RA STRAIN=mlx FVB/N;
 RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old.
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altshuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin C.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uebachs T.B., Toshikiyuki S., Carninci P., Prange C.,
 RA Bock S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Hellon E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
 RA Kravinsky M.I., Skalka U., Smalins D.E., Schermer A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RA SEQUENCE FROM N.A.
 RA STRAIN=mlx FVB/N;
 RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 RL EMBL; BC034164; AAH34164.1; -;
 DR MGD; MGI:1277201; Coll13a1.
 DR GO; GO:0005911; C:intercellular junction; IEA.
 DR InterPro; IPR008161; Clg_helix.
 DR InterPro; IPR008160; Collagen.
 DR Pfam; PF01391; Collagen; 5.
 DR Prodom; PD000007; Clg_helix; 1.
 KW Collagen.
 SQ SEQUENCE 565 AA; 56726 MW; DBD3FF99D670195F CRC64;

Query Match 10.1%; Score 132; DB 2; Length 565;
 Best Local Similarity 33.9%; Pred. No. 0.0043;
 Matches 38; Conservative 13; Mismatches 35; Indels 26; Gaps 6;
 QY 27 PSSASRIPKQKQAKLQREVVLDLYN-----MCLQGPAGVPRDSSPGA 71
 DB 393 PGAGEGSGSKG-AKSGPGKGEVVD-YNGSINEALQEIRTLALMGPGLPQTPPGP 450
 QY 72 NVIPGTP-----GIPGRDFKGEKGECLRESFESWTPNYKQCSMSLNYG 117
 DB 451 ---PPTPGQRBGILGPPGPHGDGKPRKGRKGDAGMSSTTPKGMASRNEG 499

RESULT 8

Q9N052
 ID 09N052 PRELIMINARY; PRT; 717 AA.
 AC 09N052;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)

FT MOD RES 109 109 Hydroxyproline (by similarity).
SQ SEQUENCE 246 AA; 25966 MW; 2F79BA1274BCB8E0 CRC64;
Query Match
Best Local Similarity 37.4%; Pred. No. 0.011;
Matches 34; Conservative 5; Mismatches 33; Indels 19; Gaps 2;
QY 5 GPPASPORLGLLLLLLLLPAPSSASEIPKQKQKQALROREVVDLYNGMCLGPGAVPG 64
DB 4 GPCQPCQCGCLLLFLPLPLRSQS-----AGCGICGMPGMPGAPG 47
QY 65 RDGS---PGANVPGTGTGIRGPGKKEKE 92
DB 48 KQGHDLGQPKGPGGIPAVPTGQPKQKGE 78

RESULT 10
ID 0902AO PRELIMINARY; PRT; 1472 AA.
AC 0902AO;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Collagen type XX alpha 1 precursor.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
NCBI_TaxID=9031;
RN NCB1
RP SEQUENCE FROM N.A.
RX MEDLINE=21303548; PubMed=11274142;
RA Koch M., Foley J.E., Hahn R., Zhou P., Burgeson R.E., Gerecke D.R.,
RT Gordon M.K.;
RT "alpha 1(X) collagen, a new member of the collagen subfamily, fibril-
associated collagens with interrupted triple helices";
RL J. Biol. Chem. 276:23120-23126(2001).
DR EMBL; AF312825; AKS8847.1; -.
DR HSP; P56199; I0C5.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR GO; GO:0006817; P:phosphate transport; IEA.
DR InterPro; IPR008161; Clg_helix.
DR InterPro; IPR008985; Cora_like_1ec_g1.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003129; TSP_N.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF01391; Collagen_4.
DR Pfam; PF00041; fn3; 6.
DR Pfam; PF00092; VWA; 1.
DR PRINTS; PRO0453; VWFADOMAIN.
DR PRODOM; PD000007; Clg_helix; 4.
DR SMART; SM00060; FN3; 6.
DR SMART; SM00210; TSPN; 1.
DR SMART; SM00327; VMA; 1.
DR PROSITE; PS50853; FN3; 6.
DR PROSITE; PS50234; VWA; 1.
KM Collagen; Signal.
FT SIGNAL 1 28
SQ SEQUENCE 1472 AA; 156903 MW; 536161579C56EFD CRC64;
Query Match
Best Local Similarity 9.4%; Score 122.5; DB 2; Length 1472;
Matches 37; Conservative 7; Mismatches 27; Indels 39; Gaps 6;
QY 3 PGGPASPRLRGLLLLLLP-----APSSASRI-----PKGKQKQALROREV 47
DB 1161 PGGPASPRLRGLLLLLLP-----PQGGPASPRLRGLLLLLLP----- 1207
QY 48 VDLNGMCLGPGAVPG-----GRDGPANVPGTGTGIRGPGKKEKE 91

DB 1208 -----GITITGPPGPPGKKEKGTGSPMGQIGPVGAGPRDGLQAGK 1252

RESULT 11
ID 08CFRO PRELIMINARY; PRT; 287 AA.
AC 08CFRO;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Similar to Clg-like.
GN Name=BC040774.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN NCB1
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932;
RA Strusberg R.L., Reingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.A., Loquellano N.A., Peters G.J., Abramson R.D., Millhys S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kerteman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Rodriguez S., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywnicki M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN NCB1
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RA Strauberg R.;
RL EMBL; BC040774; AAH40774.1; -.
DR HSP; Q60994; 1C28.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0006817; P:phosphate transport; IEA.
DR InterPro; IPR001073; Clg.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR008983; TNF_like.
DR Pfam; PF00386; Clg; 1.
DR Pfam; PF01391; Collagen; 1.
DR PRINTS; PRO0007; COMPLEMENTC1Q.
DR SMART; SM00110; C1Q; 1.
DR PROSITE; PS01113; C1Q; 1.
KM Collagen.
SQ SEQUENCE 287 AA; 29292 MW; 8FF89EC1C7420415 CRC64;
Query Match
Best Local Similarity 9.2%; Score 120; DB 2; Length 287;
Matches 42; Conservative 10; Mismatches 57; Indels 12; Gaps 4;
QY 27 PSSASRIIPKQKQKQALROREV-DIYNG---MCLGPGAVPGRDGSGANVTPGTGIPG 82
DB 44 PAKAKAPPPGPPSTAL---EYWDLSANPPPPFLOGPGRGPKGPGPPGPPGPPG 100
QY 83 RGFNGKEGECLERESFESWTPNYKQCSWSSIANGIDLGKIAECTFTPKRMSNSALRLPLS 142
DB 101 PGPPEKEDSGRPL-----PGLDITTSAAAGVGVVSGGTGGGDTGEGVTSLSAAPS 155

QY 143 G 143
DB 156 G 156

RESULT 12

007265 PRELIMINARY; PRT; 1752 AA.
ID 007265
AC 007265;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE 3 alpha procollagen.
GN Name=COL3A1alpha;
OS Strongylocentrotus purpuratus (Purple sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
OC Strongylocentrotus.
OX NCBI_TaxID=7668;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93186842; PubMed=8444899;
RA Exposito J.-Y., D'Alessio M., Di Liberto M., Ramirez F.;
RT "Complete primary structure of a sea-urchin type IV collagen and
RT analysis of the 5' end of its gene."
RL J. Biol. Chem. 268:5249-5254(1993).
DR EMBL; L02917; AAA30039.1; -.
DR HSSP; P02462; ILTI.
DR GO; GO:0005581; C:collagen; IEA.
DR GO; GO:0005737; C:cycloplasm; IEA.
DR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
DR GO; GO:0006817; P:phosphate transport; IEA.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR001442; Procollagen_C.
DR Pfam; PF01413; C4; 2.
DR Pfam; PF01391; Collagen; 25.
DR SMART; SM00111; C4; 2.
DR Collagen.
KW SEQUENCE 1752 AA; 170210 MW; 1AB5AAA21569346D CRC64;

Query Match 9.2%; Score 120; DB 2; Length 1752;
Best Local Similarity 22.4%; Pred. No. 0.19;
Matches 46; Conservative 20; Mismatches 61; Indels 78; Gaps 9;
QY 3 PGPASAPQRLRLLLLLQLLPASSASIRPKGKQKQALQKQREVVLDYNGMCLQGAPGV 62
DB 1453 PGPSPRDRG-----PGPQ3-----PPG-----LTGDKGT 1477
QY 63 PGRDGSFGANVIRPTGIPGRDGFKEKGECLRESF-----ESWT 103
DB 1478 PGVQGNPGVSGVGEPELKBQCFRGQNGQPPGFPRTKGEAGIRGSSGFFITRHSOT 1537
QY 104 PNYKQC-----SW-----SSLNVGIDLGKIAECTFTMRNSALRVLFSSGLRL 147
DB 1538 TSIPOCPQGTAKMHWGYSLLFVQGNRGRGQDLGKQSGC-----LKRFTMPPLFC-NINN 1592
QY 148 KCRNACCQRRYFTFNAGCSGPIPI 172
DB 1593 VCHVASRNDYSYWLSTTE---PMPM 1614

RESULT 13

018799 PRELIMINARY; PRT; 289 AA.
ID 018799
AC 018799;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-JAN-1998 (T-EMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Hypothetical protein C53B4.5.
GN Name=C53B4.5;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.

OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=9069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology."
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Berke M.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z68215; CA92453.1; -.
DR PIR; T20177; T20177.
DR WormRep; C53B4.5; C530391.
DR GO; GO:0005737; C:cycloplasm; IEA.
DR GO; GO:0042302; F:structural constituent of cuticle; IEA.
DR GO; GO:0006817; P:phosphate transport; IEA.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR002486; Col_cuticle_N.
DR Pfam; PF01391; Collagen; 2.
DR Pfam; PF01484; Col_cuticle_N; 1.
KW Collagen; Hypothetical protein.
SQ SEQUENCE 289 AA; 28993 MW; 2999A3FF9CC0B044 CRC64;

Query Match 9.1%; Score 119; DB 2; Length 289;
Best Local Similarity 34.5%; Pred. No. 0.028;
Matches 29; Conservative 5; Mismatches 20; Indels 30; Gaps 2;
QY 25 PAPSASIRPKGKQKQALQKQREVVLDYNGMCLQGAPGVGRGS-----P 69
DB 203 PPGSGSPGRPGQPS-----RGAPGQKQAGCGEKGKANGEPGP 247
QY 70 GANVIRPTGIPGRDGFKEKGEK 93
DB 248 GRDQGRGRGQGRDGRGKGC 271

RESULT 14

06MEY7
ID 06MEY7; PRELIMINARY; PRT; 358 AA.
AC 06MEY7;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN ORFNames=pc0138;
OS Parachlamydia sp. (strain UWE25) (subsp. Acanthamoeba sp.).
OC Bacteria; Chlamydiae; Chlamydiales; Parachlamydiaceae; Parachlamydia.
OX NCBI_TaxID=264201;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=null;
RA Horn M., Collingro A., Schmitz-Esser S., Beier C.L., Purkhold U.,
RA Fartmann B., Brandt P., Nyakatura G.T., Droge M., Frishman D.,
RA Rattei T., Mewes H.-W., Wagner M.;
RT "Genome sequence of an amoeba symbiont and its use for reconstructing
RT the evolutionary history of chlamydiae."
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX908798; CAF22862.1; -.
DR InterPro; IPR008160; Collagen.
DR Pfam; PF01391; Collagen; 1.
KW Hypothetical protein.
SQ SEQUENCE 358 AA; 37332 MW; 87419BD361E3D61B CRC64;

Query Match 9.1%; Score 118.5; DB 2; Length 358;
Best Local Similarity 28.1%; Pred. No. 0.04;
Matches 45; Conservative 15; Mismatches 73; Indels 27; Gaps 5;
QY 34 PPGKQKQALQKQREVVLDYNGMCLQGAPGVGRDGSFGANVIRPTGIPGRDGFKEKGC-- 91

Db 136 PPGQATGPGPPGTGEGAGLTGTGATGTLTGADGPGADGMSGSKLT 195
 QY 92 -----ECLRESFEESWTPNY-----KQCSMSLNYGIDLGKIAE-----CTF 128
 Db 196 GATGTLGATGTLTGAGPAGNNYFAYGIETGVSPVNLSPDVCPILDGWRPTNTTF 255
 QY 129 TKRRSNSALRVLFSGSLRLKCRNACCQRYWFTFNGACSCG 168
 Db 256 TCKQTGIYL-VQVRGQFTLNVMDATCALM-ATFNGSQVEG 293

RESULT 15

CAF22862 PRELIMINARY; PRT; 358 AA.
 ID CAF22862
 AC CAF22862;
 DT 14-APR-2004 (TrEMBLrel. 27, Created)
 DT 14-APR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 14-APR-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 GN PC0138.
 OS Parachlamydia sp. UME25.
 OC Bacteria; Chlamydiae; Chlamydiales; Parachlamydiaceae; Parachlamydia.
 OX NCBI_TaxID=264201;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=UME25;
 RA Horn M., Collingro A., Schmitz-Esser S., Beier C.L., Purkhold U.,
 RA Fartmann B., Brandt P., Nyakatura G.J., Droege M., Frishman D.,
 RA Rattei T., Mewes H., Wagner M.,
 RT "Genome sequence of an amoeba symbiont and its use for reconstructing
 RT the evolutionary history of chlamydiae."
 RU Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=UME25;
 RA Horn M., Collingro A., Schmitz-Esser S., Beier C.L., Purkhold U.,
 RA Fartmann B., Brandt P., Nyakatura G.J., Droege M., Frishman D.,
 RA Rattei T., Mewes H., Wagner M.,
 RU Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BX908798; CAF22862.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 358 AA; 37332 MW; 87419BD361E3D61B CRC64;

Query Match 9.1%; Score 118.5; DB 2; Length 358;
 Best Local Similarity 28.1%; Pred.No.0.04; Mismatches 73; Indels 27; Gaps 5;

Matches 45; Conservative 15; Mismatches 73; Indels 27; Gaps 5;
 QY 34 PKGKQKQLRQREVVDLYNGMCIQGPAGVGRDGSFGANVIRPTPGIDGRDGFKEBKG-- 91
 Db 136 PPGQATGPGPPGTGEGAGLTGTGATGTLTGADGPGADGMSGSKLT 195
 QY 92 -----ECLRESFEESWTPNY-----KQCSMSLNYGIDLGKIAE-----CTF 128
 Db 196 GATGTLGATGTLTGAGPAGNNYFAYGIETGVSPVNLSPDVCPILDGWRPTNTTF 255
 QY 129 TKRRSNSALRVLFSGSLRLKCRNACCQRYWFTFNGACSCG 168
 Db 256 TCKQTGIYL-VQVRGQFTLNVMDATCALM-ATFNGSQVEG 293

Search completed: December 25, 2004, 05:28:01
 Job time : 100 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 25, 2004, 03:56:15 / Search time 23 Seconds
(without alignments)
1016.551 Million cell updates/sec

Title: US-10-063-734-122

Perfect score: 1301

Sequence: 1 MRPGPASPQRRLGILL...GDASTGMSVSRRIIEELPK 243

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	122.5	9.4	246	2	S29328 complement subcomp
2	120	9.2	1752	2	A45407 collagen alpha 3(I)
3	119	9.1	289	2	T20177 hypothetical prote
4	118.5	9.1	1464	1	CGH01S collagen alpha 1(I)
5	117	9.0	327	2	T29031 hypothetical prote
6	117	9.0	754	2	A55267 collagen alpha 5(I)
7	116	8.9	888	2	S28791 collagen alpha 1(X)
8	116	8.9	1670	1	CGH03B collagen alpha 3(I)
9	115.5	8.9	1669	1	CGH04B collagen alpha 1(I)
10	115	8.8	1466	1	CGH07L collagen alpha 1(I)
11	115	8.8	1763	2	S16366 collagen alpha 2(I)
12	114.5	8.8	311	2	T15268 hypothetical prote
13	114	8.8	304	2	T26185 hypothetical prote
14	114	8.8	304	2	T26184 hypothetical prote
15	114	8.8	1691	2	S22917 collagen alpha 5(I)
16	113.5	8.7	300	2	T24482 hypothetical prote
17	113.5	8.7	920	2	A45748 collagen alpha 1(V)
18	113.5	8.7	1549	2	I48103 type VII collagen
19	113.5	8.7	1691	2	CGH06B collagen alpha 6(I)
20	113	8.7	2944	1	AS4849 collagen alpha 1(V)
21	112	8.6	178	2	A39762 collagen alpha 1(X)
22	112	8.6	325	2	T18594 hypothetical prote
23	111.5	8.6	428	2	T24769 hypothetical prote
24	111	8.5	245	1	C1H0C complement subcomp
25	111	8.5	358	2	T26281 hypothetical prote
26	110.5	8.5	298	2	T27644 hypothetical prote
27	110.5	8.5	310	2	T29731 hypothetical prote
28	110.5	8.5	458	2	T31631 hypothetical prote
29	110.5	8.5	671	1	CGRT1S collagen alpha 1(I)

30	110.5	8.5	1453	2	S21626 collagen alpha 1(I)
31	110	8.5	298	2	JCI448 collagen col-34 -
32	110	8.5	299	2	T29956 hypothetical prote
33	110	8.5	1042	1	CGCH1S collagen alpha 1(I)
34	110	8.5	1049	1	CGBO7S collagen alpha 1(I)
35	110	8.5	1568	2	T09074 hemaphorin recepto
36	110	8.5	1806	1	CGH01E collagen alpha 1(X)
37	109.5	8.4	177	2	S37749 collagen alpha 2(X)
38	109.5	8.4	290	2	T24586 collagen alpha 1(X)
39	109.5	8.4	330	2	S46657 collagen alpha 1(X)
40	109.5	8.4	488	2	A27353 collagen alpha 1(I)
41	109	8.4	1414	1	S23809 collagen alpha 2(I)
42	109	8.4	1418	2	T45467 collagen alpha 1(I)
43	109	8.4	1669	1	CGMS4B collagen alpha 1(I)
44	109	8.4	1744	2	SA0991 collagen alpha 1(I)
45	108.5	8.3	323	2	A61396 collagen alpha 1(I)

ALIGNMENTS

RESULT 1

S29328 complement subcomponent C1q chain C - mouse

C/Species: Mus musculus (house mouse)

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C/Accession: S29328

R/Petty, F.; Reid, K.B.M.; Loos, M.

Eur. J. Biochem. 209, 129-134, 1992

A/Title: Isolation, sequence analysis and characterization of cDNA clones coding for the ecerberellin.

A/Reference number: S29328; MUID:93011118; PMID:1396691

A/Accession: S29328

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-246 <PEP>

A/Cross-references: UNIPROT:002105; EMBL:X66295; NID:G50228; PIDD:CAA46993.1; PIDD:G50229

C/Superfamily: complement subcomponent C1q chain A; complement C1q carboxyl-terminal hom

F;122-245/Domain: complement C1q carboxyl-terminal homology <C1Q>

Query Match 9.4%; Score 122.5; DB 2; Length 246;

Best Local Similarity 37.4%; Pred. No. 0.0015;

Matches 34; Conservative 5; Mismatches 33; Indels 19; Gaps 2;

QY	5	GPASPRKRGILLILLQLPAPSSASERPKKQKQKLRQREVLDLNGMCGPAGVPG 64
DB	4	GPSCPQCGLCILLFLPLLRSQAS-----AGCYGPGMPGMPGAPG 47
QY	65	RDGS---PGANVTPGTPGIGRDFKGEKGE 92
DB	48	KDGHDLQSPKGPBGIPAVPTGQPKGQKGE 78

RESULT 2

A45407 collagen alpha 3 (IV) chain - sea urchin (Strongylocentrotus purpuratus)

C/Species: Strongylocentrotus purpuratus (purple urchin)

C/Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C/Accession: A45407; A43903; A23940

R/Exposito, J.Y.; D'Alessio, M.; Di Liberto, M.; Ramirez, F.

J. Biol. Chem. 268, 5249-5254, 1993

A/Title: Complete primary structure of a sea urchin type IV collagen alpha chain and ana

A/Reference number: A45407; MUID:93186842; PMID:8444895

A/Accession: A45407

A/Status: preliminary; not compared with conceptual translation

A/Molecule type: nucleic acid

A/Residues: 1-1752 <EXP>

A/Cross-references: UNIPROT:026312

A/Note: sequence extracted from NCBI backbone (NCBIP:126841)

R/Wessel, G.W.; Etkin, M.; Benson, S.

Dev. Biol. 148, 261-272, 1991

A/Title: Primary mesenchyme cells of the sea urchin embryo require an autonomously produc

A/Reference number: A43903; MUID:92038439; PMID:1936564

A:Accession: A43903
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 'P', 633-1537, 'G', <WES>
 A:Cross-references: GB:S64572; NID:G238616; PIDN:AA82070.1; PID:G238617
 A>Note: Sequence extracted from NCBI backbone (NCBIN:64572, NCBI:64573)
 R:Venkatesan, M.; De Pablo, F.; Vogeli, G.; Simpson, R.T.
 Proc. Natl. Acad. Sci. U.S.A. 83, 3351-3355, 1986
 A:Title: Structure and developmentally regulated expression of a Strongylocentrotus purp
 A:Reference number: A23940; MUID:86205894; PMID:3458186
 A:Accession: A23940
 A:Molecule type: DNA
 A:Residues: 742-812 <VEN>
 A:Cross-references: EMBL:M13206
 C:Superfamily: collagen alpha 1(IV) chain
 F:29-161/Domain: amino-terminal matrix: glycoprotein; trimer; triple helix
 F:162-1523/Region: interrupted helical
 F:1524-1752/Domain: carboxyl-terminal nonhelical, NC1 <NC1>
 F:1534-1634/Domain: collagen IV carboxyl-terminal repeat <CT1>
 F:1644-1748/Domain: collagen IV carboxyl-terminal repeat <CT2>
 F:159/Modified site: allylsine (lys) #status predicted

Query Match 9.2%; Score 120; DB 2; Length 1752;
 Best Local Similarity 22.4%; Pred. No. 0.024;
 Matches 46; Conservative 20; Mismatches 61; Indels 78; Gaps 9;

QY 3 PGPAPSPORLRLGLLTLTLTPAPSSASRIPKQKQALQREVVLDYNGMCLQGPAGV 62
 DB 1453 PGPBPGDGR-----PQPG-----PQ-----LTDDKGT 1477
 QY 63 PGRDGPANVITPTPIPRDGFKEGECLEBSF-----ESWT 103
 DB 1478 PGIQGNPVGSGVGEPELAKGEQFRGQGPDPGPGTKEAGIRPGSSGPFITHSQT 1537
 QY 104 PNYKQC-----SW-----SLNYGIDLGKIAECFTMRNSALRVFSSSLK 147
 DB 1538 TSIPPCPGTAKMHWGSLFLVQGNRGRHGDGKFGSC-----LKRSTMPFLFC-NINN 1592
 QY 148 KCRNACCCQWYTFPNAGCGSLPT 172
 DB 1593 VCHVASRNDYSYWLSTTE--PWFM 1614

RESULT 3

T20177
 hypochelical protein C53B4.5 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T20177
 R:Berks, M.
 submitted to the EMBL Data Library, December 1995
 A:Reference number: Z19233
 A:Accession: T20177
 A:Molecule type: DNA
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Residues: 1-289 <WLD>
 A:Cross-references: UNIPROT:Q18799; EMBL:Z68215; PIDN:CAA92453.1; GSEPD:GN00022; CESP:CS
 C:Experimental source: clone C53B4
 C:Genetics:
 A:Gene: CESP:C53B4.5
 A:Map position: 4

Query Match 9.1%; Score 119; DB 2; Length 289;
 Best Local Similarity 34.5%; Pred. No. 0.0038;
 Matches 29; Conservative 5; Mismatches 20; Indels 30; Gaps 2;

QY 25 PAPSASRIPKQKQALQREVVLDYNGMCLQGPAGVGRDGS-----P 69
 DB 203 PGPSPBPGDGR-----RGPAGPGRDGAQGGGKANGGPGGP 247
 QY 70 GANVITPTPIPRDGFKEGEC 93

DB 248 GRDGPGRPGPGRDGHPEKGV 271

RESULT 4

CGH15
 N:Alternate names: procollagen alpha 1(I) chain
 C:Species: Homo sapiens (man)
 C:Date: 12-Aug-1981 #sequence_revision 04-Oct-1996 #text_change 09-Jul-2004
 C:Accession: I60114, S01143, A93335, I55254, A39943, I55237, A35233, S09400, B90567, S11
 5269, A29439, I53466, A02852, I37247
 R:D'Alessio, M.; Bernard, M.; Pretorius, P.J.; de Wet, W.; Ramirez, F.; Pretorius, P.J.
 Gene 67, 105-115, 1988
 A:Title: Complete nucleotide sequence of the region encompassing the first twenty-five ex
 A:Reference number: I60114; MUID:88329734; PMID:2843432
 A:Accession: I60114
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-369, 'L', 371-589 <DAL>
 A:Cross-references: UNIPROT:P02452; UNIPROT:Q14992; UNIPROT:Q16053; UNIPROT:Q13896; UNIP
 R:Tromp, G.; Kuivaniemi, H.; Stacey, A.; Shikata, H.; Baldwin, C.T.; Jaenisch, R.; Prock
 Biochem. J. 253, 919-922, 1988
 A:Title: Structure of a full-length cDNA clone for the prepro-alpha-1(I) chain of human t
 A:Reference number: S01143; MUID:89025644; PMID:3178743
 A:Accession: S01143
 A:Molecule type: mRNA
 A:Residues: 1-472 <TRO>
 A:Cross-references: EMBL:X07884; NID:G30015; PIDN:CAA30731.1; PID:G30016; GB:M36546; NID
 A>Note: Submitted to the EMBL/Genbank/DBJ databases by Prock, D.J., 13-JUN-1988
 R:Chu, M.L.; de Wet, W.; Bernard, M.; Ding, J.F.; Morabito, M.; Myers, J.; Williams, C.;
 Nature 310, 337-340, 1984
 A:Title: Human procollagen(I) collagen gene structure reveals evolutionary conservation of
 A:Reference number: A93335; MUID:84270697; PMID:6462220
 A:Accession: A93335
 A:Molecule type: DNA
 A:Residues: 1-58, 'Q', 60-181 <CHU>
 A:Cross-references: EMBL:X00820; NID:G35657; PIDN:CAA25394.1; PID:G35658
 J:Rosow, C.M.S.; Vergier, W.P.; du Plooy, S.C.; Bernard, M.P.; Ramirez, F.; de Wet, W.;
 J. Biol. Chem. 262, 15151-15157, 1987
 A:Title: DNA sequences in the first intron of the human pro-alpha 1(I) collagen gene emb
 A:Reference number: I55254; MUID:88033098; PMID:2822714
 A:Accession: I55254
 A:Status: translation not shown; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-45 <ROS>
 A:Cross-references: GB:J02829; NID:G180387; PIDN:AAA51993.1; PID:G180388
 R:Bornstein, F.; McKay, J.; Morishima, J.K.; Devareyalu, S.; Gelinas, R.E.
 Proc. Natl. Acad. Sci. U.S.A. 84, 8869-8873, 1987
 A:Title: Regulatory elements in the first intron contribute to transcriptional control of
 A:Reference number: A39943; MUID:88097389; PMID:3480516
 A:Accession: A39943
 A:Molecule type: DNA
 A:Residues: 1-34 <BOR>
 A:Cross-references: GB:J03559; NID:G180876; PIDN:AAA52052.1; PID:G553238
 R:Chu, M.L.; de Wet, W.; Bernard, M.; Ramirez, F.
 J. Biol. Chem. 260, 2315-2320, 1985
 A:Title: Fine structural analysis of the human pro-alpha 1(I) collagen gene. Promoter st
 A:Reference number: I55237; MUID:85130970; PMID:2857713
 A:Accession: I55237
 A:Status: translation not shown; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-34 <CH2>
 A:Cross-references: GB:M10627; NID:G180383; PIDN:AAA51992.1; PID:G553226
 R:Wirtz, M.K.; Keene, D.R.; Hori, H.; Glanville, R.W.; Seidmann, B.; Rao, V.H.; Holliste
 J. Biol. Chem. 265, 6312-6317, 1990
 A:Title: In vivo and in vitro noncovalent association of excised alpha1(I) amino-terminal
 A:Reference number: A35233; MUID:90202908; PMID:2318855
 A:Accession: A35233
 A:Molecule type: protein
 A:Residues: 33-52 <WIR>
 A>Note: this propeptide fragment remained non-covalently bound to a defective, uncleaved
 R:Well, D.; d'Alessio, M.; Ramirez, F.; de Wet, W.; Cole, W.G.; Chan, D.; Bateman, J.F.

EMBO J. 8, 1705-1710, 1989
 A>Title: A base substitution in the exon of a collagen gene causes alternative splicing
 A/Reference number: S09400; MUID:89356643; PMID:2167050
 A/Accession: S09400
 A/Molecule type: mRNA
 A/Residues: 156-183 <ME1>
 R/Click, E.M.; Bornstein, P.
 Biochemistry 9, 4699-4706, 1970
 A>Title: Isolation and characterization of the cyanogen bromide peptides from the alpha1
 A/Reference number: A90567; MUID:71038625; PMID:5529814
 A/Contents: CNBx0-1, CNBx2, CNBx4, CNBx5
 A/Accession: B90567
 A/Molecule type: protein
 A/Residues: 162-198, 'Z', 200-201, 'Z', 203-206, 'Z', 208-209, 'Z', 211-228, 'B', 230, 'B', 233, 'Z'
 A/Experimental source: skin
 A/Note: evidence for 170-alanine
 R/Baerger, B.; Nodboom, H.; Diebold, J.; Lehmann, H.; Bodo, M.; Deutzmann, R.; Mueller, F.
 Eur. J. Biochem. 192, 153-159, 1990
 A>Title: A critical crosslink region in human-bone-derived collagen type I. Specific cle
 A/Reference number: S11372; MUID:90382436; PMID:2169412
 A/Accession: S11372
 A/Molecule type: protein
 A/Residues: 175-187, 274-287, 'P', 289 <BAE>
 A/Note: sequence of collagen alpha 1(S) (I) isolated from bone after pepsin digestion
 R/Deak, S.B.; Scholz, P.M.; Amenta, P.S.; Constantinou, C.D.; Levi-Manzi, S.A.; Gonzalez
 J. Biol. Chem. 266, 21827-21832, 1991
 A>Title: The substitution of arginine for glycine 85 of the alpha 1(I) procollagen chain
 A/Reference number: S15342; MUID:92042092; PMID:1718984
 A/Accession: S15342
 A/Molecule type: protein
 A/Status: translated from GB/EMBL/DBJ
 A/Residues: 258-268, 1347-1357 <DEA>
 A/Cross-references: GB:S67495; NID:G239007; PIDN:AA20350.1; PID:G239008
 A/Note: sequences from the 5' and 3' ends only are shown; mutant sequence 263-Arg report
 R/Morgan, P.H.; Jacobs, H.G.; Segrest, J.P.; Cunningham, L.W.
 J. Biol. Chem. 245, 5042-5048, 1970
 A>Title: Comparative study of glycopeptides derived from selected vertebrate collagens.
 A/Reference number: A92069; MUID:71001508; PMID:4319110
 A/Accession: A92069
 A/Molecule type: protein
 A/Residues: 263-268 <MOR>
 A/Experimental source: skin
 R/Labhard, M.E.; Hollister, D.W.
 Matrix 10, 124-130, 1990
 A>Title: Segmental amplification of the entire helical and telopeptide regions of the CD
 A/Reference number: S15989; MUID:90326017; PMID:2374517
 A/Accession: S15989
 A/Molecule type: mRNA
 A/Residues: 281-302, 402-420, 823-843, 925-944, 1026-1045, 1143-1162 <LAB>
 R/Wirt, M.K.; Rao, V.H.; Glaville, R.W.; Labhard, M.E.; Pretorius, P.J.; de Vries, W.N.
 Connect. Tissue Res. 29, 1-11, 1993
 A>Title: A cysteine for glycine substitution at position 175 in an alpha 1 (I) chain of
 A/Reference number: S15205; MUID:93339042; PMID:8339541
 A/Accession: S15205
 A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 342-352, 'C', 354-359 <W12>
 A/Cross-references: GB:S64717; NID:G408195; PIDN:AA27677.1; PID:G408196
 A/Note: mutant sequence from patient with osteogenesis imperfecta
 R/Bernard, M.P.; Chu, M.L.; Wiers, J.C.; Ramirez, F.; Ekenberry, E.F.; Prockop, D.J.
 Biochemistry 22, 5213-5223, 1983
 A>Title: Nucleotide sequences of complementary deoxyribonucleic acids for the proalpha1
 A/Reference number: A90476; MUID:84080385; PMID:6689127
 A/Accession: A90476
 A/Molecule type: mRNA
 A/Residues: 425-1250, 'X', 1252-1328, 'S', 1330-1390, 'X', 1392-1464 <BER>
 A/Cross-references: GB:K01228; NID:G180391; PIDN:AA51995.1; PID:G180392
 A/Note: sequence partially completed for missing nucleotides by A29439
 R/Chu, M.L.; Gargiulo, V.; Williams, C.J.; Ramirez, F.
 J. Biol. Chem. 260, 691-694, 1985
 A>Title: Multexon deletion in an osteogenesis imperfecta variant with increased type I

A/Reference number: A22161; MUID:85104934; PMID:2981843
 A/Accession: A22161
 A/Molecule type: DNA
 A/Residues: 472-594, 'R', 596-607 <CH3>
 A/Cross-references: GB:K03178; GB:K03179, NID:G179612; NID:G179613; PIDN:AA51847.1; PID:
 A/Note: the authors translated the codon CGT for residue 595 as Pro
 R/Wallis, G.A.; Starman, B.J.; Zimm, A.B.; Byers, P.H.
 Am. J. Hum. Genet. 46, 1034-1040, 1990
 A>Title: Variable expression of osteogenesis imperfecta in a nuclear family is explained
 A/Reference number: A35336; MUID:90252792; PMID:2339700
 A/Accession: A35336
 A/Molecule type: mRNA
 A/Residues: 710-720, 'E', 722-737, 'E', 739-745 <WAL>
 A/Note: the authors translated the codons CAG for 721 and CGT for 738 as Glu
 R/Fiorino, A.; Zolozzi, F.; Valli, M.; Pignatelli, P.F.; Cetra, G.; Brunelli, P.C.; Motres,
 Hum. Mol. Genet. 3, 2201-2206, 1994
 A>Title: Severe (type III) osteogenesis imperfecta due to glycine substitutions in the ce
 A/Reference number: S15435; MUID:95187161; PMID:7881420
 A/Accession: S15435
 A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 746-766, 'S', 768-781 <FOR>
 A/Cross-references: GB:I47667; NID:G1009093; PIDN:AA59576.1; PID:G1009094
 R/Chesler, S.D.; Wallis, G.A.; Byers, P.H.
 J. Biol. Chem. 268, 18218-18225, 1993
 A>Title: Mutations in the carboxyl-terminal propeptide of the pro alpha 1(I) chain of ty
 A/Reference number: A47426; MUID:93352646; PMID:8348697
 A/Accession: A47426
 A/Molecule type: mRNA
 A/Residues: 1179-1276, 'H', 1278-1336, 1339-1387, 'R', 1389-1464 <CHE>
 A/Cross-references: GB:S64596; NID:G407589; PIDN:AA27856.1; PID:G407590
 A/Note: sequence extracted from NCBI backbone (NCBIN:136444, NCBI:136445)
 A/Note: does not represent an experimentally determined sequence but three different mut
 A/Accession: B47426
 A/Molecule type: mRNA
 A/Residues: 1179-1464 <CH4>
 A/Experimental source: normal dermal fibroblast culture
 A/Accession: C47426
 A/Molecule type: mRNA
 A/Residues: 1179-1276, 'H', 1278-1464 <CH5>
 A/Experimental source: fetal cell 86-237
 A/Accession: D47426
 A/Molecule type: mRNA
 A/Residues: 1179-1336, 1339-1464 <CH6>
 A/Experimental source: fetal cell 86-146
 A/Accession: E47426
 A/Molecule type: mRNA
 A/Residues: 1179-1387, 'R', 1389-1464 <CH7>
 A/Experimental source: fetal cell 88-251
 R/Conn, D.H.; Apone, S.; Byre, D.R.; Starman, B.J.; Andreasen, P.; Charbonneau, H.; Nicl
 J. Biol. Chem. 263, 14605-14607, 1988
 A>Title: Substitution of Cysteine for glycine within the Carboxyl-terminal Telopeptide of
 A/Reference number: S15269; MUID:89008319; PMID:3170557
 A/Accession: S15269
 A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1187-1194, 'C', 1196-1220 <COH>
 A/Cross-references: GB:M23213; NID:G340842; PIDN:AA59363.1; PID:G499622
 A/Note: mutant sequence from a patient with mild osteogenesis imperfecta
 R/Axelrod, J.K.; Raasina, M.; Vitra, A.; Vuorio, E.
 Nucleic Acids Res. 16, 349, 1988
 A>Title: Human pro-alpha-1(I) collagen: cDNA sequence for the C-propeptide domain.
 Query Match 9.1%; Score 118.5; DB 1; Length 1464;
 Best local Similarity 36.3%; Pred. No. 0.027;
 Matches 33; Conservative 2; Mismatches 23; Indels 33; Gaps 4;
 QY 3 PGGPAA--PQRLGILLULLQLPAPSSASIPKQKQARQREVDVLYNGMCLQGA 60
 DB 357 PGGPAA--PQRLGILLULLQLPAPSSASIPKQKQARQREVDVLYNGMCLQGA 60
 QY 61 GVGGRGSPGANVYIPETPGIPGRDGFKEKG 91

Db 386 GNPAGADGPGANGANGAGIAGAPGPARG 416

RESULT 5

T29031
hypothetical protein F53G12.7 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T29031
R/Mu, X.; Graves, T.
submitted to the EMBL Data Library, May 1997
A/Description: The sequence of C. elegans cosmid F53G12.
A/Reference number: 220555
A/Accession: T29031
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-327 <MUT>
A/Cross-references: UNIPROT:O01799, EMBL:AF003139, PDB:AA54156.1, GSPDB:GN00019, CESP:
A/Experimental source: strain Bristol N2, clone F53G12
C/Genetics:
A/Gene: CESP:F53G12.7
A/Map position: 1
A/Introns: 59/3; 138/1; 223/2

Query Match
Best Local Similarity 9.0%; Score 117; DB 2; Length 327;
Matches 31; Conservative 2; Mismatches 22; Indels 38; Gaps 3;

Db 1 MRPGAPASQRLRGILLILLQLPAPSSASEIPKQKQAKLRQREVVDLYNGMCLQGPA 60
261 MGPGP-----PGPPG---PRGDKA-----GGRK 282
QY 61 GVPGRDSSPGANVPGTPGIPGRDGFGEKGEK 93
Db 283 GAFGDQGNPGPYKPGQPGAPDGSAGEKGC 315

RESULT 6

A55267
collagen alpha 5(IV) chain - dog (fragment)
C/Species: Canis lupus familiaris (dog)
C/Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004
C/Accession: A55267
R/Zheng, X.; Thorner, P.S.; Marrano, P.; Baumal, R.; McInnes, R.R.
Proc. Natl. Acad. Sci. U.S.A. 91, 3989-3993, 1994
A/Title: Canine X chromosome-linked hereditary nephritis: a genetic model for human X-1
en type IV.
A/Reference number: A55267; MUID:94224868; PMID:8171024
A/Accession: A55267
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-754 <ZHS>
A/Cross-references: UNIPROT:Q28247, GB:U07888, NID:9469547, PDB:AA60258.1, PID:9469548
C/Superfamily: collagen alpha 1(IV) chain

Query Match
Best Local Similarity 9.0%; Score 117; DB 2; Length 754;
Matches 33; Conservative 7; Mismatches 34; Indels 22; Gaps 4;

QY 3 PGGAPASQRLRGILLILLQLPAPSSASEIP-----KGKO--KAQLRQREVVDLYNGMCL 55
Db 332 PGGPPGR-----GLPGEPRGRGLPGNGIGRNGNGGCGQCPGLPGLKGD-- 377
QY 56 LQGPAGVPGRDSSPGANVPGTPGIPGRDGFGEKGEK 91
Db 378 -GGPPGIGNPGRGLNGMKDPLPGVPGPFGMKG 412

RESULT 7
S28791
collagen alpha 1(XI) chain - chicken (fragment)
C/Species: Gallus gallus (chicken)

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C/Accession: S28791
R/Nah, H.D.; Barenbaum, M.; Upholt, W.B.

J. Biol. Chem. 267, 22581-22586, 1992
A/Title: The chicken alpha 1(XI) collagen gene is widely expressed in embryonic tissues.
A/Reference number: S28791; MUID:93054557; PMID:1429607
A/Accession: S28791
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-888 <NAH>

A/Cross-references: UNIPROT:Q90796, EMBL:M88593, NID:9211619, PDB:AAA48707.1, PID:92116
C/Superfamily: collagen alpha 1(V) chain; fibrillar collagen carboxyl-terminal homology
F/655-887/Domain: fibrillar collagen carboxyl-terminal homology <FCC>

Query Match
Best Local Similarity 8.9%; Score 116; DB 2; Length 888;
Matches 31; Conservative 4; Mismatches 20; Indels 36; Gaps 3;

QY 3 PGGAPASQRLRGILLILLQLPAPSSASEIPKQKQAKLRQREVVDLYNGMCLQGPA 60
Db 479 PGGAPGKPGPEGLRGI-----PGVGE-----QLP 504
QY 61 GVPGRDSSPGANVPGTPGIPGRDGFGEKGEK 91
Db 505 GAFGDQGNPGPYKPGQPGAPDGSAGEKGC 535

RESULT 8

CGHUB3
collagen alpha 3(IV) chain precursor, long splice form - human
N/Alternate names: Goodpasture antigen, procollagen alpha 3(IV) chain long splice form
C/Species: Homo sapiens (man)
C/Date: 28-Oct-1994 #sequence_revision 03-Oct-1995 #text_change 09-Jul-2004
C/Accession: A54763; A43928; A44043; A45971; A39786
R/Mariyama, M.; Leinonen, A.; Mochizuki, T.; Tryggvason, K.; Reeders, S.T.
J. Biol. Chem. 269, 23013-23017, 1994
A/Title: Complete primary structure of the human alpha3(IV) collagen chain. Coexpression
A/Reference number: A54763; MUID:94364994; PMID:8083201
A/Accession: A54763
A/Molecule type: mRNA
A/Residues: 1-1670 <MAR>

A/Cross-references: UNIPROT:Q01955; GB:X80031, NID:9577563; PID:9577564
R/Turner, N.; Mason, P.J.; Brown, R.; Fox, M.; Povey, S.; Reese, A.; Puey, C.D.
J. Clin. Invest. 89, 592-601, 1992
A/Title: Molecular cloning of the human Goodpasture antigen demonstrates it to be the alpha
A/Reference number: A43928; MUID:92147878; PMID:1737849
A/Accession: A43928
A/Molecule type: mRNA
A/Residues: 1331-1524, 'I', 1526-1670 <TUR>

A/Cross-references: GB:M81379
R/Experimental source: Kidney
J. Quinones, S.; Bernal, D.; Garcia-Sogo, M.; Elena, S.F.; Saus, J.
J. Biol. Chem. 267, 19780-19784, 1992
A/Title: Exon/intron structure of the human alpha 3(IV) gene encompassing the Goodpasture

cton.
A/Reference number: A44043; MUID:93015826; PMID:1400291
A/Accession: A44043
A/Molecule type: DNA; mRNA

A/Residues: 1386-1670 <QUT>
A/Cross-references: GB:M92993, NID:9177895; PDB:AAA21610.1; PID:9177896
R/Note: sequence extracted from NCBI backbone (NCBI:P115597)
J. Quinones, S.; Bernal, D.; Garcia-Sogo, M.; Elena, S.F.; Saus, J.
J. Biol. Chem. 269, 17358-17359, 1994
A/Reference number: A44738; MUID:94274734; PMID:8006044

A/Content: annotation; extracut; correction to intronic sequence in A44043
R/Bernal, D.; Quinones, S.; Saus, J.
J. Biol. Chem. 268, 12090-12094, 1993
A/Title: The human mRNA encoding the Goodpasture antigen is alternatively spliced.

A/Reference number: A45971; MUID:93280184; PMID:8505332
A/Accession: A45971
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA

A:Residues: 1427-1444 <BER>
A:Note: sequence extracted from NCBI backbone (NCBIP:133363); sequence incorrectly ident
R:Morrisson, K.E.; Maruyama, M.; Yang-Feng, T.L.; Reeder, S.T.
Am. J. Hum. Genet. 49, 545-554, 1991
A:Title: Sequence and localization of a partial cDNA encoding the human alpha3 chain of
A:Reference number: A39786; MUID:91353570; PMID:1882840
A:Accession: A39786
A:Molecule type: mRNA
A:Residues: 1453-1593 'A', 1595-1670 <MOR>
A:Cross-references: GB:S55790; NID:8234418; PIDN:AA19637.1; PID:8234419
A:Comment: Prolines and lysines at the third position of the tripeptide repeating unit
ed and subsequently O-glycosylated.
C:Comment: In Goodpasture's syndrome, an autoimmune response develops against an epitope
C:Function:
A:Gene: GDB:COL4A3
A:Cross-references: GDB:128351; OMIM:120070
A:Map position: 2q36-2q37
A:Introns: 1385/1; 1418/1; 1468/1; 1547/2; 1585/3; 1643/2 #status incomplete
A:Note: the alpha 3 (IV) and alpha 4 (IV) chain genes are encoded on opposite strands with
C:Complex: This minor type IV collagen is thought to form a heterotrimer of two alpha 3
among trimer amino-terminal domains (with disulfide and desmosine cross-links), dimeric
er associations in the interrupted helical domain (with disulfide and desmosine cross-
C:Function:
A:Description: minor structural component of extracellular basement membrane in kidney
A:Superfamily: collagen alpha 1 (IV) chain
C:Keywords: alternative splicing; basement membrane; cell binding; coiled coil; extracel
F:1-28/Domain: signal sequence #status predicted <SIG>
F:129-1670/Product: collagen alpha 3 (IV) chain, long splice form #status predicted <MAT>
F:129-42/Domain: amino-terminal nonhelical, NH1 <NH1>
F:143-1438/Region: interrupted helical
F:191-793/Region: cell attachment (R-G-D) motif
F:196-998/Region: cell attachment (R-G-D) motif
F:1154-1156/Region: cell attachment (R-G-D) motif
F:11306-1308/Region: cell attachment (R-G-D) motif
F:11345-1347/Region: cell attachment (R-G-D) motif
F:1432-1434/Region: cell attachment (R-G-D) motif
F:1433-1670/Domain: carboxyl-terminal nonhelical, NCI <NCI>
F:1451-1551/Domain: collagen IV carboxyl-terminal repeat <CT1>
F:1561-1665/Domain: collagen IV carboxyl-terminal repeat <CT2>
F:131,33,39,41,125,422,476,479,682,722,809,1387/Disulfide bonds: interchain #status predi
F:253/Binding site: carboxydicte (Asn) (covalent) #status predicted
F:1460-1548, 1493-1551/Disulfide bonds: (or 1460-1551, 1493-1548) #status predicted
F:1505-1511, 1616-1622/Disulfide bonds: #status predicted
F:1570-1662, 1604-1665/Disulfide bonds: (or 1570-1665, 1604-1662) #status predicted

Query Match 8.9%; Score 116; DB 1; Length 1670;
Best Local Similarity 35.1%; Pred. No. 0.052;
Matches 33; Conservative 6; Mismatches 37; Indels 18; Gaps 3;

QY 5 GPAAQRGRKRLLLLLLPAPSSASEIPKQKQKQKQREVVVDLYNGMCQCPAGVPG 64
Db 467 GPAGEP-----GLCTCCPYIPPGPGLPGLHGVKGIPIR-----QGAAGLKG 511
QY 65 RDGSPGANVYPTGPIGRD---GFGKGECELR 95
Db 512 SPGSPGNTGLPGRPPRFGAGCGDGLKGEKGTITQ 545

RESULT 9
CGHU4B
collagen alpha 1 (IV) chain precursor - human
N:Alternate names: procollagen alpha 1 (IV) chain
C:Species: Homo sapiens (man)
C:Date: 28-May-1986 #status revision 31-Dec-1992 #text change 09-Jul-2004
C:Accession: S16876; A21117; S02738; S00048; S25826; A23115; S00207; S39614; A02863; A58
R:Solhinen, R.; Huotari, M.; Ganguly, A.; Prockop, D.J.; Trygvaason, K.
J. Biol. Chem. 264, 13565-13571, 1989
A:Title: Structural organization of the gene for the alpha-1 chain of human type IV coll
A:Reference number: S16876; MUID:89340433; PMID:2701944
A:Accession: S16876
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1669 <SO1>

A:Cross-references: UNIPROT:P02462; EMBL:J04217; GB:J05039; NID:9180800; PIDN:AAA53098.1;
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1988
R:Solhinen, R.; Huotari, M.; Hostikka, S.L.; Prockop, D.J.; Trygvaason, K.
J. Biol. Chem. 263, 17217-17220, 1988
A:Title: The structure of the alpha1 and alpha2 chains of human type IV collagen are
A:Reference number: A92690; MUID:89034231; PMID:3182844
A:Accession: A32117
A:Molecule type: DNA
A:Residues: 1-28 <SO12>
A:Cross-references: EMBL:J04217; NID:9180759; PIDN:AAA53097.1; PID:9553233
R:Poesschl, E.; Pollner, R.; Kuehn, K.
EMBO J. 7, 2687-2695, 1988
A:Title: The genes for the alpha1 (IV) and alpha2 (IV) chains of human basement membrane
A:Reference number: S02738; MUID:89030632; PMID:2846280
A:Accession: S02738
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-6, 'L', '8-28 <POS>
A:Cross-references: EMBL:X12784; NID:930072
R:Brazel, D.; Oberhauser, I.; Dieringer, H.; Babel, W.; Glanville, R.W.; Deutzmann, R.;
Eur. J. Biochem. 168, 529-536, 1987
A:Title: Completion of the amino acid sequence of the alpha1 chain of human basement memt
A:Reference number: S00048; MUID:88029471; PMID:3311751
A:Accession: S00048
A:Molecule type: mRNA
A:Residues: 1-318, 'A', 320-944 <BRA1>
A:Cross-references: EMBL:X05561; NID:930066; PIDN:CAA29075.1; PID:930067
A:Accession: S25826
A:Molecule type: protein
A:Residues: 271-318, 'A', 320-554 <BRA2>
R:Glanville, R.W.; Qian, R.Q.; Siebold, B.; Risteli, J.; Kuehn, K.
Eur. J. Biochem. 152, 213-219, 1985
A:Title: Amino acid sequence of the N-terminal aggregation and cross-linking region (7S
A:Reference number: A23115; MUID:86004708; PMID:4043082
A:Accession: A23115
A:Molecule type: protein
A:Residues: 28-236, 'KE', 239-240, 'K', 242-243 <GLA>
A:Experimental source: placenta
A:Note: the amino end of the mature form is blocked
R:Solhinen, R.; Haka-Ristku, T.; Prockop, D.J.; Trygvaason, K.
FEBS Lett. 225, 188-194, 1987
A:Title: Complete primary structure of the alpha(1)-chain of human basement membrane (ty
A:Reference number: S00207; MUID:88083584; PMID:3691802
A:Accession: S00207
A:Molecule type: mRNA
A:Residues: 244-530 <SO13>
A:Cross-references: EMBL:Y00706; NID:929548; PIDN:CAA68698.1; PID:929549
R:Edle, J.A.; Golbluk, R.; Mann, K.; Kuehn, K.
EMBO J. 12, 4795-4802, 1993
A:Title: The alpha-1-beta-1 integrin recognition site of the basement membrane collagen n
A:Reference number: S39614; MUID:94038963; PMID:8223488
A:Accession: S39614
A:Molecule type: protein
A:Residues: 371-554 <EBL>
R:Babel, W.; Glanville, R.W.
Eur. J. Biochem. 143, 545-556, 1984
A:Title: Structure of human basement-membrane (type IV) collagen. Complete amino-acid seq
A:Reference number: A02863; MUID:85003629; PMID:6434307
A:Accession: A02863
A:Molecule type: protein
A:Residues: 534-718, 'D', 720-836, 'Y', 838-841, 'P', 843-903, 'Q', 905-913, 'K', 915-997, 'K', 999-1
A:Experimental source: placenta
R:Glanville, R.W.; Rauter, A.
Hoppe-Seyler's Z. Physiol. Chem. 362, 943-951, 1981
A:Title: Peptide fragments of human placental basement-membrane collagens showing interrupt
A:Reference number: S16908; MUID:82005835; PMID:6792033
A:Accession: A58517
A:Molecule type: protein
A:Residues: 534-537, 'G', 539, 'G', 541-542, 'X', 544-553, 1389-1405, 'XX', 1408-1409, 'X', 1411-141
R:MacWhiggin, R.S.; Benson, V.A.; Lovellio, K.T.; van der Rest, M.; Fietzek, P.P.
Biochemistry 22, 4940-4948, 1983
A:Title: Isolation and characterization of pepsin-solubilized human basement membrane (ty
A:Reference number: S16910; MUID:84053346; PMID:6416291

Biochemistry 16, 1158-1164, 1977
 A>Title: Covalent structure of collagen: amino acid sequence of cyanogen bromide peptide
 A:Reference number: A90399; PMID:77134724; PMID:557335
 A:Accession: A90399
 A:Molecule type: protein
 A:Residues: 'V', 169-225, 229-232, 'P', 234-292, 'D', 294-398 <SEV1>
 A:Experimental source: liver
 A>Note: sequence corrected by A94562; attachment of 2-O-alpha-D-glucosyl-O-beta-D-galact
 R:Sever, J.M.
 submitted to the Atlas, December 1977
 A:Reference number: A94562
 A:Accession: A94562
 A:Molecule type: protein
 A:Residues: 'V', 169-225, 229-277, 'A', 279-292, 'D', 294, 'S', 296-398 <SEV2>
 A:Experimental source: liver
 A>Note: author submitted corrections to A90399
 R:Milwicz, D.M.; Mitz, A.M.; Smith, A.C.; Manchester, D.K.; Waldestein, G.; Byers, P.H.
 Am. J. Hum. Genet. 53, 62-70, 1993
 A>Title: Parental somatic and germ-line mosaicism for a multiexon deletion with unusual
 karyotyping.
 A:Reference number: 151868; PMID:93304430; PMID:8317500
 A:Accession: 151868
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 186-194 <MTL>
 A:Cross-references: GB:S62925; NID:G386425; PIDN:AAJ3937.1; PID:G4261637
 R:Chiodo, A.A.; Silience, D.O.; Cole, W.G.; Bateman, J.F.
 Biochem. J. 311, 939-943, 1995
 A>Title: Abnormal type III collagen produced by an exon-17-skipping mutation of the COL3
 A:Reference number: S59511; PMID:96067614; PMID:7487954
 A:Accession: S59511
 A:Molecule type: mRNA
 A:Residues: 302-423 <CHI>
 A:Cross-references: GB:S79877; NID:G1195576; PIDN:AA835615.1; PID:G1195577
 R:Sever, J.M.; Kang, A.H.
 Biochemistry 17, 3404-3411, 1978
 A>Title: Covalent structure of collagen: amino acid sequence of five consecutive CNBR pe
 A:Reference number: A90414; PMID:79000343; PMID:687591
 A:Accession: A90414
 A:Molecule type: protein
 A:Residues: 399-675, 'N', 677-727 <SEV3>
 A:Experimental source: liver
 R:Sever, J.M.; Vitalize, E.; Superti-Furga, A.; Steinmann, B.; Ramirez, F.
 J. Biol. Chem. 266, 5256-5259, 1991
 A>Title: G to T transversion at position +5 of a splice donor site causes skipping of th
 A:Reference number: 155349; PMID:91161621; PMID:1672129
 A:Accession: 155349
 A:Molecule type: DNA
 A:Status: translated from GB/EMBL/DBJ
 A:Residues: 537-605 <LEB>
 A:Cross-references: GB:M59112; NID:G180815; PIDN:AAA52041.1; PID:G180816
 R:Sever, J.M.; Mainardi, C.; Kang, A.H.
 Biochemistry 19, 1583-1589, 1980
 A>Title: Covalent structure of collagen: amino acid sequence of alpha1 (III)-CB5 from ty
 A:Reference number: A90438; PMID:80198282; PMID:6246925
 A:Accession: A90438
 A:Molecule type: protein
 A:Residues: 728-895, 'A', 897-964 <SEV4>
 A:Experimental source: liver
 R:Sever, J.M.; Chiodo, A.A.; Lamande, S.R.; Janeczko, R.; Ramirez, F.; Dahl, H.H.M.; Char
 J. Biol. Chem. 265, 17070-17077, 1990
 A>Title: A base substitution at a splice site in the COL3A1 gene causes exon skipping an
 A:Reference number: A38303; PMID:91009133; PMID:2145268
 A:Accession: A38303
 A:Molecule type: mRNA
 A:Residues: 861-1015 <COL>
 A:Cross-references: GB:J05617; GB:M55603; GB:M59227; NID:G180878; PIDN:AA859383.1; PID:G
 A>Note: a mutant sequence with 942-977 spliced out from a patient with Ehlers-Danlos syn
 R:Manico, B.S.; Dalgleish, R.
 Nucleic Acids Res. 16, 2337, 1988
 A>Title: Human pro alpha1(III) collagen: cDNA sequence for the 3' end.
 A:Reference number: S02119; PMID:88189827; PMID:3357782
 A:Accession: S02119

A:Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 950-1018, 'Y', 1020-1183, 'S', 1185-1466 <MAN>
 A:Cross-references: EMBL:X06700; NID:G310053; PIDN:CAA29886.1; PID:G310054
 R:Sever, J.M.; Kang, A.H.
 Biochemistry 20, 2621-2627, 1981
 A>Title: Covalent structure of collagen: amino acid sequence of alpha1 (III)-CB9 from ty
 A:Reference number: A90446; PMID:81208139; PMID:7016180
 A:Accession: A90446
 A:Molecule type: protein
 A:Residues: 965-979, 'A', 981-984, 'PS', 987, 'QN', 990-1096, 'P', 1098-1152, 'AT', 1155, 'S', 1157-1
 A:Experimental source: liver
 R:Sever, J.M.; Brinker, J.M.; May, M.; Pihlajaniemi, T.; Morrow, S.; Rosenbloom, J.; Myer
 Nucleic Acids Res. 12, 9383-9394, 1984
 A>Title: Molecular cloning and carboxyl-propeptide analysis of human type III procollagen
 A:Reference number: A93551; PMID:85087944; PMID:6096827
 A:Accession: A93551
 A:Molecule type: mRNA
 A:Residues: 1065-1155, 'P', 1157-1466 <LOI>
 A:Cross-references: EMBL:X01655; EMBL:X01742; NID:G29584; PIDN:CAA25821.1
 R:Wiskuln, M.; Dalgleish, R.; Kluge-Beckman, B.; Renard, S.I.; Tolstoshev, P.; Brant
 Biochemistry 25, 1408-1413, 1986
 A>Title: Human type III collagen gene expression is coordinately modulated with the type
 A:Reference number: 152393; PMID:86187804; PMID:3754462
 A:Accession: 152393
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1161-1200 <MS>
 A:Cross-references: GB:M1146; NID:G180415; PIDN:AA52003.1; PID:G180416
 R:Emmanuel, B.S.; Cammizaro, L.A.; Sever, J.M.; Myers, J.C.
 Proc. Natl. Acad. Sci. U.S.A. 82, 3385-3389, 1985
 A>Title: Human alpha 1(III) and alpha 2(V) procollagen genes are located on the long arm
 A:Reference number: 159025; PMID:85156505; PMID:3858826
 A:Accession: 179339
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1165-1196 <ENA>
 A:Cross-references: GB:M1134; NID:G180417; PIDN:AA52004.1; PID:G180418
 R:Chu, M.L.; Weil, D.; de Wet, W.; Bernard, M.; Stippola, M.; Ramirez, F.
 J. Biol. Chem. 260, 4357-4363, 1985
 A>Title: Isolation of cDNA and genomic clones encoding human pro-alpha(III) collagen. P
 A:Reference number: A92516; PMID:85157600; PMID:2579949
 A:Accession: A92516
 A:Molecule type: DNA
 A:Residues: 1176-1240, 'V', 1242-1356, 'P', 1358-1466 <CHU>
 A:Cross-references: GB:M10615; GB:M10793; GB:M10794; GB:M10795; GB:M10796; GB:M10797; GB:
 A:Experimental source: liver
 A>Note: the authors translated the codon TTC for residue 1057 as Tyr; the codons given for
 action
 C:Comment: Proline and lysines at the third position of the tripeptide repeating unit (C
 3-hydroxylated. About 15% of the lysines are 5-hydroxylated and some are subsequently O-
 C:Keywords: collagen
 A:Gene: COL3A1
 A:Cross-references: GDB:118729; OMIM:120180
 A:Map position: 2q31-2q31
 A:Introns: 27/1, 94/3, 111/3, 149/3, 166/3, 554/3, 587/3, 1175/3, 1275/1, 1337/3, 1418/3
 A>Note: the list of introns is incomplete; defects in this gene can result in Ehlers-Dan
 C:Complex: type III collagen is a homotrimer of monomers initially linked by disulfide bo
 er of their length, is formed with desmosine cross-links made from lysine and allylsine re
 A:Function:
 A:Description: structural component of extracellular fibrous polymer that maintains integ
 C:Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology;
 C:Keywords: coiled coil; Ehlers-Danlos syndrome; extracellular matrix; glycoprotein; hyd
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-153/Domain: amino-terminal propeptide #status predicted <PRO>
 F:154-1221/Domain: von Willebrand factor type C repeat homology <VWC>
 F:154-1221/Product: collagen alpha 1(III) chain #status predicted <MAT>
 F:154-167/Region: amino-terminal nonhelical telopeptide
 F:168-1196/Region: helical
 F:1091-1093/Region: cell attachment (R-G-D) motif
 F:1197-1221/Region: carboxyl-terminal nonhelical telopeptide
 F:1222-1466/Domain: carboxyl-terminal propeptide #status predicted <CPR>
 F:1238-1466/Domain: fibrillar collagen carboxyl-terminal homology <FCC>

C:Accession: T26184
R:Gardner, A.
submitted to the EMBL Data Library, October 1996
A:Reference number: Z20166
A:Accession: T26184
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-304 <WIL>
A:Cross-references: UNIPROT:Q9XNG3; EMBL:Z61138; PDB:CA03474.1; GSPDB:GN00021; CESP:W0
A:Experimental source: clone W05B2
C:Genetics:
A:Gene: CESP.W05B2.6
A:Map position: 3
A:Introns: 27/3

Query Match 8.8%; Score 114; DB 2; Length 304;
Best Local Similarity 31.9%; Pred. No. 0.011;
Matches 29; Conservative 5; Mismatches 25; Indels 32; Gaps 2;

QY 3 PGPAPSPRLRLGLLLLLQLPAPSSASERPKQKQKQALRGREVVVDLYNMGMLQGPAGV 62
Db 227 PQGP-----PGPAGSPGAPGPGQAG-----APGPKGP 254

QY 63 PGRDSPGANVIFGTRPGIRGDFKGEKGC 93
Db 255 SGAPGQPGADGNRNGARCGCGSGAGKEKIC 285

RESULT 15
S22917
collagen alpha 5(IV) chain precursor, renal splice form - human
N:Alternate names: procollagen alpha 5(IV) chain
N:Contains: collagen alpha 5(IV) chain precursor, leukocyte splice form
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence, revision 27-Feb-1997 #ext change 09-Jul-2004
C:Accession: S22917; A54365; A57079; A37122; A34850; S18850; I56971; I76598; A35
R:Zhou, J.; Herter, J.M.; Leinonen, A.; Trygsvaason, K.
J. Biol. Chem. 267, 12475-12481, 1992
A:Title: Complete amino acid sequence of the human alpha-5(IV) collagen chain and identi
n Alport syndrome patient.
A:Reference number: S22917; MUID:92316923; PMID:1352287
A:Accession: S22917
A:Molecule type: mRNA
A:Residues: 1-967 <ZHO>
A:Cross-references: UNIPROT:P29400; GB:M90464; NID:G180826; PDB:AAA52046.1; PID:G553234
R:Zhou, J.; Leinonen, A.; Trygsvaason, K.
J. Biol. Chem. 269, 6608-6614, 1994
A:Title: Structure of the human type IV collagen COL4A5 gene.
A:Reference number: A54365; MUID:94165049; PMID:8120014
A:Accession: A54365
A:Molecule type: DNA
A:Residues: 1-922 <ZHO>
A:Cross-references: GB:U04470; NID:G463378; GB:U04520; NID:G463428; PDB:AA027816.1; PID
R:Zhou, J.; Mochizuki, T.; Smeets, H.; Antignac, C.; Laurilla, P.; de Paep, A.; Trygsva
Science 261, 1167-1169, 1993
A:Title: Deletion of the paired alpha5(IV) and alpha6(IV) collagen genes in inherited sm
A:Reference number: A57079; MUID:93361972; PMID:8356449
A:Accession: A57079
A:Molecule type: DNA
A:Residues: 1-27 <ZHA>
A:Cross-references: GB:Z37153; NID:G587203; PDB:CAA85512.1; PID:G587204
R:Philaient, T.; Pohjola, E.R.; Meyer, J.C.
J. Biol. Chem. 265, 13758-13766, 1990
A:Title: Complete primary structure of the triple-helical region and the carboxyl-termin
A:Reference number: A37122; MUID:90337990; PMID:2380186
A:Accession: A37122
A:Molecule type: mRNA
A:Residues: 84-439, 'GS', 442-624, 'LAIO', 629-666, 'FR', 669-887, 'R', 889-1264, 1271-1691 <PIH>
A:Cross-references: GB:U05558; EMBL:M58526; NID:G1314209
A:Note: Submitted to the EMBL Data Library, February 1991
A:Note: the authors translated the codon GGC for residue 115 as Val
R:Renieri, A.; Serri, M.; Meyer, J.C.; Philaient, T.; Massella, L.; Rizzoni, G.; De Ma
Hum. Mol. Genet. 1, 127-129, 1992

A:Title: De novo mutation in the COL4A5 gene converting glycine 325 to glutamic acid in /
A:Reference number: I54317; MUID:93244772; PMID:1363780
A:Accession: I54317
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 313-324, 'E', 326-330 <REN>
A:Cross-references: GB:S59334; NID:G299946; PDB:AA013909.1; PID:G4261609
R:Hostikka, S.L.; Eddy, R.L.; Byers, M.G.; Hoeythya, M.; Shows, T.B.; Trygsvaason, K.
Proc. Natl. Acad. Sci. U.S.A. 87, 1606-1610, 1990
A:Title: Identification of a distinct type IV collagen alpha chain with restricted kidney
A:Reference number: A34850; MUID:90160375; PMID:1689491
A:Accession: A34850
A:Molecule type: mRNA
A:Residues: 914-1264, 1271-1691 <HOS>
A:Cross-references: EMBL:M31115; NID:G180824; PDB:AAA52045.1; PID:G180825
R:Zhou, J.; Hostikka, S.L.; Chow, L.T.; Trygsvaason, K.
Genomics 9, 1-9, 1991
A:Title: Characterization of the 3' half of the human type IV collagen alpha-5 gene that
A:Reference number: A37969; MUID:91169491; PMID:2004755
A:Accession: S18850
A:Molecule type: DNA
A:Residues: 924-1264, 1271-1691 <ZHO>
A:Cross-references: EMBL:M63455; EMBL:M63456; EMBL:M63457; EMBL:M63458; EMBL:M63459; EMBL
8; EMBL:M63470; EMBL:M63471; EMBL:M63472; EMBL:M63473; NID:G177922; PDB:AAA51558.1; PID:
R:Guo, C.; Van Damme, B.; Van Damme-Lombaerts, R.; Van den Bergh, H.; Cassiman, J.J.; Me
Kidney Int. 44, 1316-1321, 1993
A:Title: Differential splicing of COL4A5 mRNA in kidney and white blood cells: a complex
A:Reference number: I56971; MUID:94133540; PMID:8301933
A:Accession: I56971
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1258-1276 <GUO1>
A:Cross-references: GB:S69168; NID:G545095; PDB:AA060612.1; PID:G545096
A:Note: Kidney splice form
A:Accession: I76598
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1284-1291, 'TRPGYLAQV' <GUO2>
A:Cross-references: GB:S69169; NID:G545097; PDB:AA060613.1; PID:G545098
A:Note: Frameshift mutation in patient with Alport syndrome
R:Myers, J.C.; Jones, T.A.; Pohjola, E.R.; Kadiri, A.S.; Goddard, A.D.; Sheer, D.; So
Am. J. Hum. Genet. 46, 1024-1033, 1990
A:Title: Molecular cloning of alpha5(IV) collagen and assignment of the gene to the regio
A:Reference number: A35335; MUID:90252791; PMID:2339699
A:Accession: A35335
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1448-1477 <MYE>
R:Nakazato, H.; Hattori, S.; Ushijima, T.; Matsura, T.; Koitabashi, Y.; Takada, T.; Yost
Kidney Int. 46, 1307-1314, 1994
A:Title: Mutations in the COL4A5 gene in Alport syndrome: a possible mutation in primordi
A:Reference number: I56975; MUID:95156893; PMID:7853788
A:Accession: I56975
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1595-1602 <NAX>
A:Cross-references: GB:S79903; NID:G913882; PDB:AA03374.1; PID:G913883
A:Note: premature termination mutation from a patient with Alport syndrome; one other mut
R:Lemink, H.H.; Schroeder, C.H.; Brunner, H.G.; Nelen, M.R.; Zhou, J.; Trygsvaason, K.; i
Genomics 17, 485-489, 1993
A:Title: Identification of four novel mutations in the COL4A5 gene of patients with Alpo
A:Reference number: I54188; MUID:94010948; PMID:8406498
A:Accession: I54188
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1604-1607, 'VHDAYXC' <LEM>
A:Cross-references: GB:S65767; NID:G425563; PDB:AA013967.1; PID:G4261667
A:Note: frameshift mutation from a patient with Alport syndrome; five other mutations are
C:Comment: Prolines and lysines at the third position of the tripeptide repeating unit (C
ed and subsequently O-glycosylated).
C:Genetics:
A:Gene: GDB:COL4A5; A35
A:Cross-references: GDB:120596; OMIM:303630

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OM protein - protein search, using sw model

Run on: December 25, 2004, 05:12:05 ; Search time 23 Seconds
(without alignments)
700.664 Million cell updates/sec

Title: US-10-063-734-122

Perfect score: 1301
Sequence: 1 MKPGPASPQRRLGILL...GPASTGMSVSRITIEELPK 243

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/1/1aa/PCOTUS_COMB.pep:*
6: /cgn2_6/prodata/1/1aa/backfile01.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1301	100.0	243	4	US-09-834-759-514 Sequence 514, App
2	1301	100.0	278	4	US-09-834-759-515 Sequence 515, App
3	1294	99.5	243	4	US-09-692-081-4 Sequence 4, Appl
4	1291	99.2	243	4	US-09-489-847-205 Sequence 205, App
5	1216	93.5	245	4	US-09-692-081-2 Sequence 2, Appl
6	1216	93.5	277	4	US-09-692-081-5 Sequence 5, Appl
7	1100.5	84.6	276	4	US-09-205-258-958 Sequence 958, App
8	1053	80.9	197	4	US-09-834-759-516 Sequence 516, App
9	1053	80.9	232	4	US-09-834-759-517 Sequence 517, App
10	356	27.4	66	4	US-09-205-258-962 Sequence 962, App
11	296	22.8	52	4	US-09-205-258-961 Sequence 961, App
12	270	20.8	51	4	US-09-205-258-963 Sequence 963, App
13	248	19.1	46	4	US-09-834-759-518 Sequence 518, App
14	211.5	16.3	52	4	US-09-205-258-960 Sequence 960, App
15	196	15.1	93	4	US-09-489-847-240 Sequence 240, App
16	196	15.1	93	4	US-09-489-847-362 Sequence 362, App
17	141	10.8	26	4	US-09-834-759-519 Sequence 519, App
18	122.5	9.4	246	2	US-08-463-911-4 Sequence 4, Appl
19	118.5	9.1	1057	3	US-08-931-820-1 Sequence 1, Appl
20	118.5	9.1	1461	4	US-09-585-887-9 Sequence 9, Appl
21	118.5	9.1	1461	4	US-09-289-578-9 Sequence 9, Appl
22	118.5	9.1	1464	4	US-09-331-347C-21 Sequence 21, Appl
23	115.5	8.9	128	3	US-09-227-357-190 Sequence 190, App
24	115	8.8	623	3	US-09-029-348-3 Sequence 3, Appl
25	115	8.8	626	3	US-09-029-348-2 Sequence 2, Appl
26	113.5	8.7	1694	1	US-08-494-168-2 Sequence 2, Appl
27	112.5	8.6	492	4	US-08-468-996-12 Sequence 12, Appl

28	112	8.6	96	4	US-09-513-999C-4206 Sequence 4206, App
29	112	8.6	208	4	US-09-800-729-151 Sequence 151, App
30	111	8.5	245	4	US-09-552-225A-4 Sequence 4, Appl
31	111	8.5	245	4	US-09-552-204A-4 Sequence 4, Appl
32	110.5	8.5	310	3	US-09-219-849-47 Sequence 47, Appl
33	110.5	8.5	595	3	US-09-219-849-48 Sequence 48, Appl
34	110.5	8.5	595	3	US-09-219-849-50 Sequence 50, Appl
35	110.5	8.5	684	1	US-08-555-663-12 Sequence 12, Appl
36	110.5	8.5	684	4	US-09-073-663-12 Sequence 12, Appl
37	110.5	8.5	755	4	US-09-919-497-57 Sequence 57, Appl
38	110.5	8.5	822	3	US-09-219-849-49 Sequence 49, Appl
39	110	8.5	258	4	US-09-976-594-815 Sequence 815, App
40	110	8.5	1568	3	US-09-181-706-2 Sequence 2, Appl
41	110	8.5	1568	3	US-09-458-791-2 Sequence 2, Appl
42	110	8.5	1568	3	US-09-459-066-2 Sequence 2, Appl
43	110	8.5	1568	4	US-09-459-066-2 Sequence 2, Appl
44	110	8.5	1806	4	US-09-919-497-56 Sequence 56, Appl
45	108.5	8.3	234	4	US-09-895-674A-1 Sequence 1, Appl

ALIGNMENTS

RESULT 1					
US-09-834-759-514					
; Sequence 514: Application US/09834759					
; Patent No. 6680197					
; GENERAL INFORMATION:					
; APPLICANT: Uiang, Yuguin					
; APPLICANT: Dillon, David C.					
; APPLICANT: Mitcham, Jennifer L.					
; APPLICANT: Xu, Jiangchun					
; APPLICANT: Harlocker, Susan L.					
; APPLICANT: Hepler, William T.					
; APPLICANT: Henderson, Robert A.					
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND					
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER					
; FILE REFERENCE: 210121.470C9					
; CURRENT APPLICATION NUMBER: US/09/834,759					
; CURRENT FILING DATE: 2001-04-13					
; NUMBER OF SEQ ID NOS: 547					
; SOFTWARE: FastSeq for Windows Version 3.0					
; SEQ ID NO 514					
; LENGTH: 243					
; TYPE: PR					
; ORGANISM: Homo sapiens					
US-09-834-759-514					
Query Match					
Best Local Similarity 100.0%; Pred. No. 9e-128;					
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1	MRPGPASPQRRLGILLQLLPAPSSASEIPKQKQAKLRREVVLDLYNGMCLQGA	60		
DB	1	MRPGPASPQRRLGILLQLLPAPSSASEIPKQKQAKLRREVVLDLYNGMCLQGA	60		
QY	61	GVPGRGSGANVIRCTPGIRPGDGRKRGKGLAREPFEESTPNYKQCSWSLNYGIDL	120		
DB	61	GVPGRGSGANVIRCTPGIRPGDGRKRGKGLAREPFEESTPNYKQCSWSLNYGIDL	120		
QY	121	GKIAECTFPKMSNSALRYLFGSLRLKCRNACCORWYTFPGAECGSLPFEATYLDQ	180		
DB	121	GKIAECTFPKMSNSALRYLFGSLRLKCRNACCORWYTFPGAECGSLPFEATYLDQ	180		
QY	181	GSPENNSTINIRTSVEGLCEGIGALVDVAIWGTCSDPKGPASTGMSVSRITIEE	240		
DB	181	GSPENNSTINIRTSVEGLCEGIGALVDVAIWGTCSDPKGPASTGMSVSRITIEE	240		
QY	241	LPR 243			
DB	241	LPR 243			

RESULT 2

US-09-834-759-515
; Sequence 515, Application US/09834759
; Patent No. 6680197
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jianshun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepner, William T.
; APPLICANT: Henderson, Robert A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C9
; CURRENT APPLICATION NUMBER: US/09/834,759
; CURRENT FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 515
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-834-759-515

Query Match 100.0%; Score 1301; DB 4; Length 278;
Best Local Similarity 100.0%; Pred. No. 1.1e-127;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPGPASPORLRGLLILLLQLPAPSSASEIPKQKQKQRLRQREVVDLYNMGCLQGPA 60
DB 36 MRPGPASPORLRGLLILLLQLPAPSSASEIPKQKQKQRLRQREVVDLYNMGCLQGPA 95
QY 61 GVPGRDSSPGANVIRPGTPIGRDGFKEGKECELRSEFSESWTPNYKQCSWSLNYGIDL 120
DB 96 GVPGRDSSPGANVIRPGTPIGRDGFKEGKECELRSEFSESWTPNYKQCSWSLNYGIDL 155
QY 121 GKIAECTFTKRSNSALRVLFSGSLRLKCRNACCORWYTFENGACSGPLPIEATIIYDQ 180
DB 156 GKIAECTFTKRSNSALRVLFSGSLRLKCRNACCORWYTFENGACSGPLPIEATIIYDQ 215
QY 181 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIIVGTCSDYKGDASTGMNSVSRITIEE 240
DB 216 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIIVGTCSDYKGDASTGMNSVSRITIEE 275
QY 241 LPK 243
DB 276 LPK 278

RESULT 3

US-09-692-081-4
; Sequence 4, Application US/09692081
; Patent No. 6630325
; GENERAL INFORMATION:
; APPLICANT: LINDNER, Volkhart
; APPLICANT: PRISESE, Robert F.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO REMODEL
; FILE REFERENCE: 36-13 Lindner et al. (200036.0013)
; CURRENT APPLICATION NUMBER: US/09/692,081
; CURRENT FILING DATE: 2000-10-19
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-692-081-4

Query Match 99.5%; Score 1294; DB 4; Length 243;
Best Local Similarity 99.6%; Pred. No. 4.9e-127;
Matches 242; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRPGPASPORLRGLLILLLQLPAPSSASEIPKQKQKQRLRQREVVDLYNMGCLQGPA 60
DB 1 MRPGPASPORLRGLLILLLQLPAPSSASEIPKQKQKQRLRQREVVDLYNMGCLQGPA 60
QY 61 GVPGRDSSPGANVIRPGTPIGRDGFKEGKECELRSEFSESWTPNYKQCSWSLNYGIDL 120
DB 61 GVPGRDSSPGANVIRPGTPIGRDGFKEGKECELRSEFSESWTPNYKQCSWSLNYGIDL 120
QY 121 GKIAECTFTKRSNSALRVLFSGSLRLKCRNACCORWYTFENGACSGPLPIEATIIYDQ 180
DB 121 GKIAECTFTKRSNSALRVLFSGSLRLKCRNACCORWYTFENGACSGPLPIEATIIYDQ 180
QY 181 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIIVGTCSDYKGDASTGMNSVSRITIEE 240
DB 181 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIIVGTCSDYKGDASTGMNSVSRITIEE 240
QY 241 LPK 243
DB 241 LPK 243

RESULT 4

US-09-489-847-205
; Sequence 205, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: P2031P1
; CURRENT APPLICATION NUMBER: US/09/489,847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 205
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-489-847-205

Query Match 99.2%; Score 1291; DB 4; Length 243;
Best Local Similarity 99.2%; Pred. No. 1e-126;
Matches 241; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRPGPASPORLRGLLILLLQLPAPSSASEIPKQKQKQRLRQREVVDLYNMGCLQGPA 60
DB 1 MRPGPASPORLRGLLILLLQLPAPSSASEIPKQKQKQRLRQREVVDLYNMGCLQGPA 60
QY 61 GVPGRDSSPGANVIRPGTPIGRDGFKEGKECELRSEFSESWTPNYKQCSWSLNYGIDL 120
DB 61 GVPGRDSSPGANVIRPGTPIGRDGFKEGKECELRSEFSESWTPNYKQCSWSLNYGIDL 120
QY 121 GKIAECTFTKRSNSALRVLFSGSLRLKCRNACCORWYTFENGACSGPLPIEATIIYDQ 180
DB 121 GKIAECTFTKRSNSALRVLFSGSLRLKCRNACCORWYTFENGACSGPLPIEATIIYDQ 180
QY 181 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIIVGTCSDYKGDASTGMNSVSRITIEE 240
DB 181 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIIVGTCSDYKGDASTGMNSVSRITIEE 240
QY 241 LPK 243
DB 241 LPK 243


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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 958
; LENGTH: 276
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (10)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-205-258-958

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Query Match      84.6%; Score 1100.5; DB 4; Length 276;
Best Local Similarity 96.7%; Pred. No. 9.7e-107;
Matches 203; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 34 PKGKQKALOREVVDLYNGMCLQGPAGVPRGDSFGANVTPGTGIRGDFKGEKGC 93
DB 68 PRG-SKRIRKREVDLYNGMCLQGPAGVPRGDSFGANVTPGTGIRGDFKGEKGC 126
QY 94 LRFSEFESWTNPKYKQCSWSLNYGIDLGKIAECTTKRSALRVLFSSGLRLKCRAC 153
DB 127 LRFSEFESWTNPKYKQCSWSLNYGIDLGKIAECTTKRSALRVLFSSGLRLKCRAC 186
QY 154 CORVYFTFNAGACGSPLEIAIITYLDQSPENNSTINIRHTSSVEGLCEGIGAGLVDAI 213
DB 187 CORVYFTFNAGACGSPLEIAIITYLDQSPENNSTINIRHTSSVEGLCEGIGAGLVDAI 246
QY 214 WVGTCSDYPRKGDASTGNMVSRIIIEELPK 243
DB 247 WVGTCSDYPRKGDASTGNMVSRIIIEELPK 276

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RESULT 8
US-09-834-759-516
; Sequence 516, Application US/09834759
; Patent No. 6680197
; GENERAL INFORMATION:

```

```

; APPLICANT: Jiang, Yugui
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jianshun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C9
; CURRENT APPLICATION NUMBER: US/09/834,759
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 516
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-834-759-516

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Query Match      80.9%; Score 1053; DB 4; Length 197;
Best Local Similarity 100.0%; Pred. No. 5.6e-102;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPGPASPORLGLLILLLILQLPAPSSASEIPKQKQALRQREVVDLYNGMCLQGPA 60
DB 1 MRPGPASPORLGLLILLLILQLPAPSSASEIPKQKQALRQREVVDLYNGMCLQGPA 60
QY 61 GVPGRDSPGANVTPGTGIRGDFKGEKGCLEARFESWTNPKYKQCSWSLNYGIDL 120
DB 61 GVPGRDSPGANVTPGTGIRGDFKGEKGCLEARFESWTNPKYKQCSWSLNYGIDL 120
QY 121 GKIAECTTKRSALRVLFSSGLRLKCRNACCQWYFTFNAGACGSPLEIAIITYLDQ 180
DB 121 GKIAECTTKRSALRVLFSSGLRLKCRNACCQWYFTFNAGACGSPLEIAIITYLDQ 180
QY 181 GSPENNSTINIRHTSSV 197
DB 181 GSPENNSTINIRHTSSV 197

```

```

RESULT 9
US-09-834-759-517
; Sequence 517, Application US/09834759
; Patent No. 6680197
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugui
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jianshun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C9
; CURRENT APPLICATION NUMBER: US/09/834,759
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 517
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-834-759-517

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Query Match      80.9%; Score 1053; DB 4; Length 232;
Best Local Similarity 100.0%; Pred. No. 7e-102;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPGPASPORLGLLILLLILQLPAPSSASEIPKQKQALRQREVVDLYNGMCLQGPA 60
DB 36 MRPGPASPORLGLLILLLILQLPAPSSASEIPKQKQALRQREVVDLYNGMCLQGPA 95

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QY 61 GVGGRDSSGANVYIPTGTGIPGRDGFKEGKGECLREPFESWTPTYKQCSWSLNYGIDL 120
DB 96 GVGGRDSSGANVYIPTGTGIPGRDGFKEGKGECLREPFESWTPTYKQCSWSLNYGIDL 155
QY 121 GKIACTPTKMSNSALRYLFGSGLRLKCRNACCORWYTFNGAECGSLPTLEAIYYLDQ 180
DB 156 GKIACTPTKMSNSALRYLFGSGLRLKCRNACCORWYTFNGAECGSLPTLEAIYYLDQ 215
QY 181 GSPENNSTINIRTSV 197
DB 216 GSPENNSTINIRTSV 232

RESULT 10
US-09-205-258-962
; Sequence 962, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; EARLIER FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
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EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 962
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-205-258-962

Query Match 27.4%; Score 356; DB 4; Length 66;
Best Local Similarity 100.0%; Pred. No. 8.3e-30;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 128 FTKMSNSALRYLFGSGLRLKCRNACCORWYTFNGAECGSLPTLEAIYYLDQSPENMS 187
DB 1 FTKMSNSALRYLFGSGLRLKCRNACCORWYTFNGAECGSLPTLEAIYYLDQSPENMS 60
QY 188 TINIR 193
DB 61 TINIR 66

RESULT 11
US-09-205-258-961
; Sequence 961, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; EARLIER FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
```

EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/049,020
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,876
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,895
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,884
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,894
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,971
 EARLIER FILING DATE: 1997-06-06
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 EARLIER FILING DATE: 1997-06-06
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 EARLIER FILING DATE: 1997-06-06
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 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,915
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/049,019
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,970
 EARLIER FILING DATE: 1997-06-06
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 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/049,373
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,875
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 EARLIER APPLICATION NUMBER: 60/048,898
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 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,963
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,877
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048,878
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/070,923
 EARLIER FILING DATE: 1997-12-18
 EARLIER APPLICATION NUMBER: 60/092,921
 EARLIER FILING DATE: 1998-07-15
 EARLIER APPLICATION NUMBER: 60/094,657
 NUMBER OF SEQ ID NOS: 1237
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 961
 LENGTH: 52

; TYPE: PRT
 ; ORGANISM: Homo sapiens
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 Best Local Similarity 100.0%; Pred. No. 1.1e-23; Mismatches 0; Indels 0; Gaps 0;
 Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Cy 77 TTPIDPGRDGFKEKGEKCEKRESEETWTNYQCSWSSLNTGIDGKIAECTF 128
 Db 1 TTPIDPGRDGFKEKGEKCEKRESEETWTNYQCSWSSLNTGIDGKIAECTF 52
 RESULT 12
 US-09-205-258-963
 ; Sequence 963, Application US/09205258
 ; Patent No. 6525174
 ; GENERAL INFORMATION:
 ; APPLICANT: Young et al.
 ; TITLE OF INVENTION: 207 Human Secreted Proteins
 ; FILE REFERENCE: P2007P1
 ; CURRENT APPLICATION NUMBER: US/09/205,258
 ; EARLIER FILING DATE: 1998-12-04
 ; EARLIER APPLICATION NUMBER: PCT/US98/11422
 ; EARLIER FILING DATE: 1998-06-04
 ; EARLIER APPLICATION NUMBER: 60/048,885
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/049,375
 ; EARLIER FILING DATE: 1997-06-06
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 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/048,896
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/049,020
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/048,876
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/048,895
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/048,884
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 ; EARLIER FILING DATE: 1997-06-06
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 ; EARLIER APPLICATION NUMBER: 60/049,373
 ; EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,875
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EARLIER FILING DATE: 1997-06-06
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EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,878
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/070,923
EARLIER FILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 963
LENGTH: 51
TYPE: PRT
ORGANISM: Homo sapiens
US-09-205-258-963

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Best Local Similarity 100.0%; Pred.No. 5,6e-21;
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RESULT 13
US-09-834-759-518
Sequence 518, Application US/09834759
Patent No. 6660197
GENERAL INFORMATION:
APPLICANT: Jiang, Yugu
APPLICANT: Dillon, David C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Xu, Jianshun
APPLICANT: Harlocker, Susan L.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121,470C9
CURRENT APPLICATION NUMBER: US/09/834,759
CURRENT FILING DATE: 2001-04-13
NUMBER OF SEQ ID NOS: 547
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 518
LENGTH: 46
TYPE: PRT
ORGANISM: Homo sapiens
US-09-834-759-518

Query Match 19.1%; Score 248; DB 4; Length 46;

Best Local Similarity 100.0%; Pred.No. 9.7e-19;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 14
US-09-205-258-960
Sequence 960, Application US/09205258
Patent No. 6525174
GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: P2007P1
CURRENT APPLICATION NUMBER: US/09/205,258
CURRENT FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: PCT/US98/11422
EARLIER FILING DATE: 1998-06-04
EARLIER APPLICATION NUMBER: 60/048,885
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,375
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EARLIER APPLICATION NUMBER: 60/048,881
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; EARLIER FILING DATE: 1997-06-06
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; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 960
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-205-258-960

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Best Local Similarity 16.3%; Score 211.5; DB 4; Length 52;
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Db 7 PRG-SKRRIRQREVVDLYNGMCLQGPAGVPGRDSPGANGIPGTPT 52

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RESULT 15
US-09-489-847-240
; Sequence 240, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: P2031P1
; CURRENT APPLICATION NUMBER: US/09/489,847
; EARLIER FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
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; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 240
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-489-847-240

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Query Match 15.1%; Score 196; DB 4; Length 93;

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Best Local Similarity 100.0%; Pred. No. 7.1e-13;
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Db 1 MRPGPASPQRULGILLILLIQLPASPASSEIRPKGXKA 40

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Search completed: December 25, 2004, 05:28:28
Job time : 24 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 25, 2004, 05:28:31 ; Search time 23 Seconds
(without alignments)
700.664 Million cell updates/sec

Title: US-10-063-734-122

Perfect score: 243
Sequence: 1 MRPGPASPQRRLGILL...GDASTGWSVSRRIIEELPK 243

Scoring table: Oligo
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size: 6
Total number of hits satisfying chosen parameters: 2312

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	243	100.0	243	US-09-834-759-514	Sequence 514, App
2	243	100.0	278	US-09-834-759-515	Sequence 515, App
3	197	81.1	197	US-09-834-759-516	Sequence 516, App
4	197	81.1	232	US-09-834-759-517	Sequence 517, App
5	170	70.0	243	US-09-692-081-4	Sequence 517, App
6	170	70.0	276	US-09-205-258-958	Sequence 958, App
7	111	45.7	245	US-09-692-081-2	Sequence 2, App11
8	111	45.7	277	US-09-692-081-5	Sequence 5, App11
9	88	36.2	243	US-09-489-847-205	Sequence 205, App
10	66	27.2	66	US-09-205-258-962	Sequence 962, App
11	52	21.4	52	US-09-205-258-961	Sequence 961, App
12	51	21.0	51	US-09-205-258-963	Sequence 963, App
13	46	18.9	46	US-09-834-759-518	Sequence 518, App
14	40	16.5	93	US-09-489-847-240	Sequence 240, App
15	40	16.5	93	US-09-489-847-362	Sequence 362, App
16	30	12.3	52	US-09-205-258-960	Sequence 960, App
17	26	10.7	26	US-09-834-759-519	Sequence 519, App
18	15	6.2	15	US-09-692-081-7	Sequence 7, App11
19	9	3.7	80	US-09-248-796A-23275	Sequence 23275, A
20	9	3.7	654	US-09-252-991A-25801	Sequence 25801, A
21	9	3.7	905	US-09-369-364A-9	Sequence 9, App11
22	9	3.7	1057	US-08-931-820-1	Sequence 1, App11
23	9	3.7	1341	US-08-963-825-18	Sequence 18, App1
24	9	3.7	1341	US-09-500-811-18	Sequence 18, App1
25	9	3.7	1341	US-09-570-573-18	Sequence 18, App1
26	9	3.7	1341	US-09-548-608-18	Sequence 18, App1
27	9	3.7	1461	US-09-585-887-9	Sequence 9, App11

28	9	3.7	1461	US-09-289-578-9	Sequence 9, App11
29	9	3.7	1464	US-09-331-347C-21	Sequence 21, App1
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36	8	3.3	71	US-09-059-625-7	Sequence 7, App1
37	8	3.3	72	US-09-059-625-4	Sequence 4, App1
38	8	3.3	74	US-09-621-976-3804	Sequence 3904, App
39	8	3.3	82	US-09-248-796A-21887	Sequence 21887, A
40	8	3.3	129	US-10-000-489-98	Sequence 98, App1
41	8	3.3	131	US-10-000-489-84	Sequence 84, App1
42	8	3.3	131	US-10-000-489-86	Sequence 86, App1
43	8	3.3	143	US-09-227-357-192	Sequence 192, App1
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45	8	3.3	151	US-09-059-625-43	Sequence 43, App1
	8	3.3	151	US-09-059-625-46	Sequence 46, App1

ALIGNMENTS

RESULT 1					
US-09-834-759-514					
Sequence 514, Application US/09834759					
Patent No. 6680197					
GENERAL INFORMATION:					
APPLICANT: Jjiang, Yugu					
APPLICANT: Dillon, Davin C.					
APPLICANT: Mitcham, Jennifer L.					
APPLICANT: Xu, Jiangchun					
APPLICANT: Harlocker, Susan L.					
APPLICANT: Hepler, William T.					
APPLICANT: Henderson, Robert A.					
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND					
FILE REFERENCE: 210121.470C9					
CURRENT APPLICATION NUMBER: US/09/834,759					
CURRENT FILING DATE: 2001-04-13					
NUMBER OF SEQ ID NOS: 547					
SOFTWARE: FastSeq for Windows Version 3.0					
SEQ ID NO 514					
LENGTH: 243					
TYPE: PRT					
ORGANISM: Homo sapiens					
US-09-834-759-514					
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Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
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QY	121	GRIACFTPKRNSALR	121	GRIACFTPKRNSALR	121
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DB	181	GSPENSTINIRTSVE	181	GSPENSTINIRTSVE	181
QY	241	LPRK 243	241	LPRK 243	241
DB	241	LPRK 243	241	LPRK 243	241

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; Sequence 515, Application US/09834759
; Patent No. 6680197
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiaqichun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C9
; CURRENT APPLICATION NUMBER: US/09/834,759
; CURRENT FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 515
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-834-759-515
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Best Local Similarity 100.0%; Pred. No. 2e-227;
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      96 GVPGRDGSFGANVITGTPGIPGRDGFKEGKECECLRESFESWTPNYKQCSWSSLYNGIDL 155
QY      121 GKIACCTFTKRSNSALNVLFSGSLRLKCRNACCCORWYTFENGAECSGGLPIEAIYYLDO 180
      156 GKIACCTFTKRSNSALNVLFSGSLRLKCRNACCCORWYTFENGAECSGGLPIEAIYYLDO 215
QY      181 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIWTGTCSDYPRKGDASTGMNSVSRITIEE 240
      216 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIWTGTCSDYPRKGDASTGMNSVSRITIEE 275
QY      241 LPK 243
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RESULT 3
US-09-834-759-516
; Sequence 516, Application US/09834759
; Patent No. 6680197
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiaqichun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C9
; CURRENT APPLICATION NUMBER: US/09/834,759
; CURRENT FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 516
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-09-834-759-516
Query Match      81.1%; Score 197; DB 4; Length 197;
Best Local Similarity 100.0%; Pred. No. 5.7e-183;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MRPOGPASPORLRGLLLLLLLQLPAPSSASEIPKQKQKQRLRQREVVDLYNMGCLQGPA 60
      36 MRPOGPASPORLRGLLLLLLLQLPAPSSASEIPKQKQKQRLRQREVVDLYNMGCLQGPA 95
QY      61 GVPGRDGSFGANVITGTPGIPGRDGFKEGKECECLRESFESWTPNYKQCSWSSLYNGIDL 120
      96 GVPGRDGSFGANVITGTPGIPGRDGFKEGKECECLRESFESWTPNYKQCSWSSLYNGIDL 155
QY      121 GKIACCTFTKRSNSALNVLFSGSLRLKCRNACCCORWYTFENGAECSGGLPIEAIYYLDO 180
      156 GKIACCTFTKRSNSALNVLFSGSLRLKCRNACCCORWYTFENGAECSGGLPIEAIYYLDO 215
QY      181 GSPENNSTINIHRTSSV 197
      216 GSPENNSTINIHRTSSV 197
DB
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RESULT 4
US-09-834-759-517
; Sequence 517, Application US/09834759
; Patent No. 6680197
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiaqichun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C9
; CURRENT APPLICATION NUMBER: US/09/834,759
; CURRENT FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 517
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-834-759-517
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Query Match      81.1%; Score 197; DB 4; Length 232;
Best Local Similarity 100.0%; Pred. No. 6.6e-183;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MRPOGPASPORLRGLLLLLLLQLPAPSSASEIPKQKQKQRLRQREVVDLYNMGCLQGPA 60
      36 MRPOGPASPORLRGLLLLLLLQLPAPSSASEIPKQKQKQRLRQREVVDLYNMGCLQGPA 95
QY      61 GVPGRDGSFGANVITGTPGIPGRDGFKEGKECECLRESFESWTPNYKQCSWSSLYNGIDL 120
      96 GVPGRDGSFGANVITGTPGIPGRDGFKEGKECECLRESFESWTPNYKQCSWSSLYNGIDL 155
QY      121 GKIACCTFTKRSNSALNVLFSGSLRLKCRNACCCORWYTFENGAECSGGLPIEAIYYLDO 180
      156 GKIACCTFTKRSNSALNVLFSGSLRLKCRNACCCORWYTFENGAECSGGLPIEAIYYLDO 215
QY      181 GSPENNSTINIHRTSSV 197
      216 GSPENNSTINIHRTSSV 232
DB
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RESULT 5
US-09-692-081-4
; Sequence 4, Application US/09692081
; Patent No. 6630325
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; GENERAL INFORMATION:
; APPLICANT: LINDNER, Volkhard
; APPLICANT: PRIESEL, Robert F
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO REMODEL
; FILE REFERENCE: 36-13 Lindner et al. (200036.0013)
; CURRENT APPLICATION NUMBER: US/09/692,081
; CURRENT FILING DATE: 2000-10-19
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 4
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-692-081-4

Query Match      70.0%; Score 170; DB 4; Length 243;
Best Local Similarity 100.0%; Pred. No. 1e-156;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 IPGTGIPGRDGFKEKKEKCELRSESPESWTPTYKOCSSSLNYGIDLGKIACTFTKMS 133
DB 74 IPGTGIPGRDGFKEKKEKCELRSESPESWTPTYKOCSSSLNYGIDLGKIACTFTKMS 133
QY 134 NSALRVLFSGSLRLKCRNACCQRMWYFTFNGAECGSLPIEAIITYDDGSPENNSTINHR 193
DB 134 NSALRVLFSGSLRLKCRNACCQRMWYFTFNGAECGSLPIEAIITYDDGSPENNSTINHR 193
QY 194 TSSVEGLCEGIGAGLVDAIWMGTGSDYKGDASTGMNSVSRITIEELPK 243
DB 194 TSSVEGLCEGIGAGLVDAIWMGTGSDYKGDASTGMNSVSRITIEELPK 243

RESULT 6
US-09-205-258-958
; Sequence 958, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 958
; LENGTH: 276
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: SITE
; LOCATION: (10)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; US-09-205-258-958

Query Match      70.0%; Score 170; DB 4; Length 276;
Best Local Similarity 100.0%; Pred. No. 1.1e-156;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 IPGTGIPGRDGFKEKKEKCELRSESPESWTPTYKOCSSSLNYGIDLGKIACTFTKMS 133
DB 107 IPGTGIPGRDGFKEKKEKCELRSESPESWTPTYKOCSSSLNYGIDLGKIACTFTKMS 166
QY 134 NSALRVLFSGSLRLKCRNACCQRMWYFTFNGAECGSLPIEAIITYDDGSPENNSTINHR 193
DB 167 NSALRVLFSGSLRLKCRNACCQRMWYFTFNGAECGSLPIEAIITYDDGSPENNSTINHR 226
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QY 194 TSSVEGLCEGIGAGLVDAIWMGTCSDPKGDASTGMNSVSRITIELPK 243
DB 227 TSSVEGLCEGIGAGLVDAIWMGTCSDPKGDASTGMNSVSRITIELPK 276

RESULT 7

US-09-692-081-2
; Sequence 2, Application US/09692081
; Patent No. 6630325
; GENERAL INFORMATION:
; APPLICANT: LINDNER, Volkhard
; APPLICANT: FRIESEL, Robert P.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO REMODEL
; FILE REFERENCE: 36-13 Lindner et al. (200036.0013)
; CURRENT APPLICATION NUMBER: US/09/692,081
; CURRENT FILING DATE: 2000-10-19
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-692-081-2

Query Match 45.7%; Score 111; DB 4; Length 245;
Best Local Similarity 100.0%; Pred. No. 1,6e-99;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 IPGPGIPGSDGFGKEGCECRESFESWTPTYKQCSWMSLNYGIDGKIAECTFTKMS 133
DB 76 IPGPGIPGSDGFGKEGCECRESFESWTPTYKQCSWMSLNYGIDGKIAECTFTKMS 135
QY 134 NSALRVLFSSGLRKCRRNACCORWYFTFNAGCSGPIPIAIIYLDGSPF 184
DB 136 NSALRVLFSSGLRKCRRNACCORWYFTFNAGCSGPIPIAIIYLDGSPF 186

RESULT 8

US-09-692-081-5
; Sequence 5, Application US/09692081
; Patent No. 6630325
; GENERAL INFORMATION:
; APPLICANT: LINDNER, Volkhard
; APPLICANT: FRIESEL, Robert P.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO REMODEL
; FILE REFERENCE: 36-13 Lindner et al. (200036.0013)
; CURRENT APPLICATION NUMBER: US/09/692,081
; CURRENT FILING DATE: 2000-10-19
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-692-081-5

Query Match 45.7%; Score 111; DB 4; Length 277;
Best Local Similarity 100.0%; Pred. No. 1,8e-99;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 IPGPGIPGSDGFGKEGCECRESFESWTPTYKQCSWMSLNYGIDGKIAECTFTKMS 133
DB 108 IPGPGIPGSDGFGKEGCECRESFESWTPTYKQCSWMSLNYGIDGKIAECTFTKMS 167
QY 134 NSALRVLFSSGLRKCRRNACCORWYFTFNAGCSGPIPIAIIYLDGSPF 184
DB 168 NSALRVLFSSGLRKCRRNACCORWYFTFNAGCSGPIPIAIIYLDGSPF 218

RESULT 9

US-09-489-847-205
; Sequence 205, Application US/09489847
; Patent No. 6476195

; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: P2031P1
; CURRENT APPLICATION NUMBER: US/09/489,847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 205
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-489-847-205

Query Match 36.2%; Score 88; DB 4; Length 243;
Best Local Similarity 100.0%; Pred. No. 3,1e-77;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 156 RMYFTFNAGCSGPIPIAIIYLDGSPFNSTINIHRTSSVEGLCEGIGAGLVDAIWM 215
DB 156 RMYFTFNAGCSGPIPIAIIYLDGSPFNSTINIHRTSSVEGLCEGIGAGLVDAIWM 215
QY 216 GTCSDYPKGDASTGMNSVSRITIELPK 243
DB 216 GTCSDYPKGDASTGMNSVSRITIELPK 243

RESULT 10

US-09-205-258-962
; Sequence 962, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,882
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,899
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,893
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,900
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,901
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,892
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,915
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,019
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,970
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,972
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,916
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,373
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,875
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,374
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,917
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,949
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,974
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,883
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,897
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,898
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,962
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,963
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,877
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,878
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/070,923
EARLIER FILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 962
LENGTH: 66
TYPE: PRT
ORGANISM: Homo sapiens
US-09-205-258-962

Query Match 27.2%; Score 66; DB 4; Length 66;
Best Local Similarity 100.0%; Pred. No. 2e-56;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 128 FTKMSNSALRYLFSSGLKCRNACCCWYFFFNAGSGSPPIRATIIYDDGSPBNMS 187
DB 1 FTKMRSNSALRYLFSSGLKCRNACCCWYFFFNAGSGSPPIRATIIYDDGSPBNMS 60
QY 188 TINHR 193

Db 61 TINHR 66
RESULT 11
US-09-205-258-961
Sequence 961, Application US/09205258
Patent No. 6525174
GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: P2007P1
CURRENT APPLICATION NUMBER: US/09/205,258
CURRENT FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: PCT/US98/11422
EARLIER FILING DATE: 1998-06-04
EARLIER APPLICATION NUMBER: 60/048,885
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,375
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,881
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,880
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,896
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,020
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,876
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,895
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,884
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,894
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,971
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,882
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,899
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,893
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,900
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,901
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,892
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,915
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,019
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,970
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,972
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,916
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,373
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,875
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,374
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,917
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,949
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,974

RESULT 13

US-09-834-759-518
; Sequence 518, Application US/09834759
; Patent No. 6680197
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C9
; CURRENT APPLICATION NUMBER: US/09/834,759
; CURRENT FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 518
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-834-759-518

Query Match 18.9%; Score 46; DB 4; Length 46;
Best Local Similarity 100.0%; Pred. No. 3.6e-37;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 198 EGIICGIGAGLVDAIIVGTCTSDYPRKGDASTGMSVSRITIIIEELPK 243
Db 1 EGIICGIGAGLVDAIIVGTCTSDYPRKGDASTGMSVSRITIIIEELPK 46

RESULT 14
US-09-489-847-240
; Sequence 240, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: P2031P1
; CURRENT APPLICATION NUMBER: US/09/489,847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 240
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-489-847-240

Query Match 16.5%; Score 40; DB 4; Length 93;
Best Local Similarity 100.0%; Pred. No. 4.4e-31;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MRPGPASPQRRLGILLILLQLPAPSSASEIPKQKQK 40

RESULT 15

US-09-489-847-362
; Sequence 362, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: P2031P1
; CURRENT APPLICATION NUMBER: US/09/489,847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 362
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-489-847-362

Query Match 16.5%; Score 40; DB 4; Length 93;
Best Local Similarity 100.0%; Pred. No. 4.4e-31;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 25, 2004, 05:29:51 ; Search time 70 Seconds

(without alignments)
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Title: US-10-063-734-122

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Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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SUMMARIES

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3	243	100.0	243	10	US-09-946-374-352
4	243	100.0	243	10	US-09-946-374-352
5	243	100.0	243	13	US-10-063-547-122
6	243	100.0	243	13	US-10-063-547-122
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9	243	100.0	243	13	US-10-063-547-122
10	243	100.0	243	14	US-10-176-759-366
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15	243	100.0	243	14	US-10-176-483-366	Sequence 366, App
16	243	100.0	243	14	US-10-176-749-366	Sequence 366, App
17	243	100.0	243	14	US-10-176-914-366	Sequence 366, App
18	243	100.0	243	14	US-10-176-915-366	Sequence 366, App
19	243	100.0	243	14	US-10-063-569-122	Sequence 122, App
20	243	100.0	243	14	US-10-063-513-122	Sequence 122, App
21	243	100.0	243	14	US-10-063-515-122	Sequence 122, App
22	243	100.0	243	14	US-10-063-512-122	Sequence 122, App
23	243	100.0	243	14	US-10-173-706-366	Sequence 366, App
24	243	100.0	243	14	US-10-175-738-366	Sequence 366, App
25	243	100.0	243	14	US-10-175-752-366	Sequence 366, App
26	243	100.0	243	14	US-10-176-482-366	Sequence 366, App
27	243	100.0	243	14	US-10-176-757-366	Sequence 366, App
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30	243	100.0	243	14	US-10-180-557-366	Sequence 366, App
31	243	100.0	243	14	US-10-076-622-514	Sequence 514, App
32	243	100.0	243	14	US-10-063-502-122	Sequence 122, App
33	243	100.0	243	14	US-10-173-700-366	Sequence 366, App
34	243	100.0	243	14	US-10-174-572-366	Sequence 366, App
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36	243	100.0	243	14	US-10-174-582-366	Sequence 366, App
37	243	100.0	243	14	US-10-174-588-366	Sequence 366, App
38	243	100.0	243	14	US-10-175-739-366	Sequence 366, App
39	243	100.0	243	14	US-10-175-743-366	Sequence 366, App
40	243	100.0	243	14	US-10-176-488-366	Sequence 366, App
41	243	100.0	243	14	US-10-176-492-366	Sequence 366, App
42	243	100.0	243	14	US-10-176-747-366	Sequence 366, App
43	243	100.0	243	14	US-10-176-750-366	Sequence 366, App
44	243	100.0	243	14	US-10-176-985-366	Sequence 366, App
45	243	100.0	243	14	US-10-176-985-366	Sequence 366, App

ALIGNMENTS

RESULT 1
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; Sequence 514, Application US/09834759
; Publication No. US20020085998A1
; GENERAL INFORMATION:
; APPLICANT: Jilgon, Yugu
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jianshun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C9
; CURRENT APPLICATION NUMBER: US/09/834,759
; CURRENT FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 514
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-834-759-514
Query Match 100.0%; Score 243; DB 9; Length 243;
Best Local Similarity 100.0%; Pred. No. 1.8e-211;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 61 GVPGRDGSFGANVIGTPTGIPGRDGFKGKGECLRESFEESWTPTVYKQCSWSLNYGIDL 120

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; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 10
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; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-938-418-7

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QY      181 GSEPNASTNIHRTSSVEGLCEGIGAGLVDAIWTGTCSDDPKGDASTGMNSVSRIITIE    240
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QY      241 LPK 243
Db      241 LPK 243

RESULT 3
US-09-946-374-352
; Sequence 352, Application US/09946374
; Publication No. US20030073129A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paonli, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C1
CURRENT APPLICATION NUMBER: US/09/946,374
PRIOR FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: 60/098716
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098723
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098749
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098750

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PRIOR APPLICATION NUMBER: 60/101014
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PRIOR FILING DATE: 1998-09-18
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PRIOR FILING DATE: 1998-10-08
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PRIOR APPLICATION NUMBER: 60/105693
PRIOR FILING DATE: 1998-10-26
PRIOR APPLICATION NUMBER: 60/105694
PRIOR FILING DATE: 1998-10-26
PRIOR APPLICATION NUMBER: 60/105807

Query Match 100.0%; Score 243; DB 10; Length 243;
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DB 181 GSPENSTINIRHTSVEGLCEIGAGLYDVAIMWGTGSDYPRGDASTGMSVRIIEE 240
QY 241 LPK 243
DB 241 LPK 243

RESULT 5
US-10-006-867-122
Sequence 122, Application US/10006867
Publication No. US20020119130A1
GENERAL INFORMATION:
APPLICANT: Eaton, Dan L.
APPLICANT: Filvaroff, Ellen
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Watanabe, Colin K.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3230R1C1
CURRENT FILING DATE: US/10/006,867
PRIOR APPLICATION NUMBER: 2001-12-06
PRIOR FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: 60/063435
PRIOR FILING DATE: 1997-10-29

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PRIOR APPLICATION NUMBER: 60/119287
PRIOR FILING DATE: 1999-02-09
PRIOR APPLICATION NUMBER: 60/119525
PRIOR FILING DATE: 1999-02-10
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PRIOR FILING DATE: 1999-02-10
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PRIOR FILING DATE: 1999-04-13
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PRIOR FILING DATE: 1999-04-16
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PRIOR FILING DATE: 1999-04-27
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PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/169495
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PRIOR APPLICATION NUMBER: 60/191007
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PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 09/380138
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 09/380142

Query Match 100.0%; Score 243; DB 13; Length 243;
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DB 241 LPK 243

RESULT 6

US-10-052-586-366
Sequence 366, Application US/10052586
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James

APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C1
CURRENT APPLICATION NUMBER: US/10/052,586
CURRENT FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
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PRIOR APPLICATION NUMBER: 60/068017
PRIOR FILING DATE: 1997-12-18
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
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PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079786
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PRIOR APPLICATION NUMBER: 60/080107
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080194
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080327
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080333
PRIOR FILING DATE: 1998-04-01

PRIOR APPLICATION NUMBER: 60/081049
 PRIOR FILING DATE: 1998-04-08
 PRIOR APPLICATION NUMBER: 60/081070
 PRIOR FILING DATE: 1998-04-08
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 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083499
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083559
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/084366
 PRIOR FILING DATE: 1998-05-05
 PRIOR APPLICATION NUMBER: 60/084414
 PRIOR FILING DATE: 1998-05-06
 PRIOR APPLICATION NUMBER: 60/084639
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084640
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 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088167
 PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/088202

PRIOR FILING DATE: 1998-06-05
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 PRIOR FILING DATE: 1998-06-05
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 PRIOR APPLICATION NUMBER: 60/088876
 PRIOR FILING DATE: 1998-06-11
 PRIOR APPLICATION NUMBER: 60/089090
 PRIOR FILING DATE: 1998-06-12
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 PRIOR APPLICATION NUMBER: 60/089514
 PRIOR FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: 60/089538
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089598
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089653
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089908

Query Match 100.0%; Score 243; DB 13; Length 243;
 Best Local Similarity 100.0%; Pred. No. 1,8e-211; Mismatches 0; Indels 0; Gaps 0;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPGPAPSPORLRLGLLLLLQLPAPSSASEIPKQKQAOUREVVDLYNMCLOGPA 60
 Db 1 MRPGPAPSPORLRLGLLLLLQLPAPSSASEIPKQKQAOUREVVDLYNMCLOGPA 60
 QY 61 GVPGRDSSPQANVTPTGPIPRDGFKEGEGCLRESEESWTPTYKQCSWSLNYGIDL 120
 Db 61 GVPGRDSSPQANVTPTGPIPRDGFKEGEGCLRESEESWTPTYKQCSWSLNYGIDL 120
 QY 121 GKIAECTFTKMSNSALRYLPSGSLRLKCRNACCORWFTNGAECCGPPIEMIIYLDQ 180
 Db 121 GKIAECTFTKMSNSALRYLPSGSLRLKCRNACCORWFTNGAECCGPPIEMIIYLDQ 180
 QY 181 GSPENASTINIRHTSSVEGLCEGIGAGLVDAIIVWGTCSDPYKGDASTGNNVSRIIIEE 240
 Db 181 GSPENASTINIRHTSSVEGLCEGIGAGLVDAIIVWGTCSDPYKGDASTGNNVSRIIIEE 240
 QY 241 LPK 243
 Db 241 LPK 243

RESULT 7
 US-10-007-805-514
 ; Sequence 514, Application US/10007805


```
Publication No. US20020150581A1
GENERAL INFORMATION:
APPLICANT: Jiang Yugu
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Xu, Jiangchun
APPLICANT: Harlocker, Susan L.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: McNeill, Patricia D.
APPLICANT: Durham, Margalita
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.470C10
CURRENT APPLICATION NUMBER: US/10/007, 805
CURRENT FILING DATE: 2001-12-07
NUMBER OF SEQ ID NOS: 593
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 514
LENGTH: 243
TYPE: PRT
ORGANISM: Homo sapiens
US-10-007-805-514

Query Match 100.0%; Score 243; DB 13; Length 243;
Best Local Similarity 100.0%; Pred. No. 1.8e-211;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPGPAASPORLRLGLLLLLLLQLPAPSSASEIPKQKQAOQRORREVDVLYNMGCLQGRA 60
DB 1 MRPGPAASPORLRLGLLLLLLLQLPAPSSASEIPKQKQAOQRORREVDVLYNMGCLQGRA 60
QY 61 GVGGRDSSPGANVYIPETPGIPGRDGFKEGKGECLRESFEESWTPNYKQCSWSLNYGIDL 120
DB 61 GVGGRDSSPGANVYIPETPGIPGRDGFKEGKGECLRESFEESWTPNYKQCSWSLNYGIDL 120
QY 121 GKIAECTFTKMSNSALRYLFGSGLRLKCRNACCORWYFTFNGAECGSPLEAIYYLDQ 180
DB 121 GKIAECTFTKMSNSALRYLFGSGLRLKCRNACCORWYFTFNGAECGSPLEAIYYLDQ 180
QY 181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDAIWTGCSDPYKGDASTGMNSVSRITIEE 240
DB 181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDAIWTGCSDPYKGDASTGMNSVSRITIEE 240
QY 241 LPK 243
DB 241 LPK 243

RESULT 8
US-10-063-547-122
Sequence 122, Application US/10063547
Publication No. US20020182638A1
GENERAL INFORMATION:
APPLICANT: Eaton, Dan L.
APPLICANT: Filvaroff, Ellen
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3230R1C1
CURRENT APPLICATION NUMBER: US/10/063, 547
CURRENT FILING DATE: 2002-05-02
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 122
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LENGTH: 243
TYPE: PRT
ORGANISM: Homo Sapien
US-10-063-547-122

Query Match 100.0%; Score 243; DB 13; Length 243;
Best Local Similarity 100.0%; Pred. No. 1.8e-211;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPGPAASPORLRLGLLLLLLLQLPAPSSASEIPKQKQAOQRORREVDVLYNMGCLQGRA 60
DB 1 MRPGPAASPORLRLGLLLLLLLQLPAPSSASEIPKQKQAOQRORREVDVLYNMGCLQGRA 60
QY 61 GVGGRDSSPGANVYIPETPGIPGRDGFKEGKGECLRESFEESWTPNYKQCSWSLNYGIDL 120
DB 61 GVGGRDSSPGANVYIPETPGIPGRDGFKEGKGECLRESFEESWTPNYKQCSWSLNYGIDL 120
QY 121 GKIAECTFTKMSNSALRYLFGSGLRLKCRNACCORWYFTFNGAECGSPLEAIYYLDQ 180
DB 121 GKIAECTFTKMSNSALRYLFGSGLRLKCRNACCORWYFTFNGAECGSPLEAIYYLDQ 180
QY 181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDAIWTGCSDPYKGDASTGMNSVSRITIEE 240
DB 181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDAIWTGCSDPYKGDASTGMNSVSRITIEE 240
QY 241 LPK 243
DB 241 LPK 243
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RESULT 9
US-10-063-551-122
Sequence 122, Application US/10063551
Publication No. US20020183494A1
GENERAL INFORMATION:
APPLICANT: Eaton, Dan L.
APPLICANT: Filvaroff, Ellen
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3230R1C1
CURRENT APPLICATION NUMBER: US/10/063, 551
CURRENT FILING DATE: 2002-05-02
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 122
LENGTH: 243
TYPE: PRT
ORGANISM: Homo Sapien
US-10-063-551-122

Query Match 100.0%; Score 243; DB 13; Length 243;
Best Local Similarity 100.0%; Pred. No. 1.8e-211;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPGPAASPORLRLGLLLLLLLQLPAPSSASEIPKQKQAOQRORREVDVLYNMGCLQGRA 60
DB 1 MRPGPAASPORLRLGLLLLLLLQLPAPSSASEIPKQKQAOQRORREVDVLYNMGCLQGRA 60
QY 61 GVGGRDSSPGANVYIPETPGIPGRDGFKEGKGECLRESFEESWTPNYKQCSWSLNYGIDL 120
DB 61 GVGGRDSSPGANVYIPETPGIPGRDGFKEGKGECLRESFEESWTPNYKQCSWSLNYGIDL 120
QY 121 GKIAECTFTKMSNSALRYLFGSGLRLKCRNACCORWYFTFNGAECGSPLEAIYYLDQ 180
DB 121 GKIAECTFTKMSNSALRYLFGSGLRLKCRNACCORWYFTFNGAECGSPLEAIYYLDQ 180
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QY 181 GSPENNSTINIRHTSSVEGLCEGIGAGLVDAIHWGTCSDYKDGASTGMSVSRIITIEE 240
DB 181 GSPENNSTINIRHTSSVEGLCEGIGAGLVDAIHWGTCSDYKDGASTGMSVSRIITIEE 240
QY 241 LPK 243
DB 241 LPK 243

RESULT 10

US-10-174-590-366
; Sequence 366, Application US/10174590
; Publication No. US20030008352A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Auecin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C142
; CURRENT APPLICATION NUMBER: US/10/174,590
; PRIOR APPLICATION DATE: 2002-06-18
; PRIOR APPLICATION REMOVED - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 366
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-174-590-366

Query Match 100.0%; Score 243; DB 14; Length 243;
Best Local Similarity 100.0%; Pred. No. 1.8e-211;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPGPASPQRIRGLILLILLQLPAPSSASEIPKQKQAKLRQREVDLYNMGCLQGPA 60
DB 1 MRPGPASPQRIRGLILLILLQLPAPSSASEIPKQKQAKLRQREVDLYNMGCLQGPA 60
QY 61 GVPGRDGSFGANVTPGTPIGPDGFGKEGECLEARSFESWTPTNYKQCSWSLNYGIDL 120
DB 61 GVPGRDGSFGANVTPGTPIGPDGFGKEGECLEARSFESWTPTNYKQCSWSLNYGIDL 120
QY 121 GKIAECTFTKRSNSALRYLFGSGLRLKCRNACCQRYWTFPGAECGSPLEAIITVYDQ 180
DB 121 GKIAECTFTKRSNSALRYLFGSGLRLKCRNACCQRYWTFPGAECGSPLEAIITVYDQ 180
QY 181 GSPENNSTINIRHTSSVEGLCEGIGAGLVDAIHWGTCSDYKDGASTGMSVSRIITIEE 240
DB 181 GSPENNSTINIRHTSSVEGLCEGIGAGLVDAIHWGTCSDYKDGASTGMSVSRIITIEE 240
QY 241 LPK 243
DB 241 LPK 243

RESULT 11

US-10-176-758-366
; Sequence 366, Application US/10176758
; Publication No. US20030008353A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Auecin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C104
CURRENT APPLICATION NUMBER: US/10/176,758
PRIOR APPLICATION DATE: 2002-06-21
PRIOR APPLICATION REMOVED - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 366
LENGTH: 243
TYPE: PRT
ORGANISM: Homo Sapien
US-10-176-758-366

Query Match 100.0%; Score 243; DB 14; Length 243;
Best Local Similarity 100.0%; Pred. No. 1.8e-211;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPGPASPQRIRGLILLILLQLPAPSSASEIPKQKQAKLRQREVDLYNMGCLQGPA 60
DB 1 MRPGPASPQRIRGLILLILLQLPAPSSASEIPKQKQAKLRQREVDLYNMGCLQGPA 60
QY 61 GVPGRDGSFGANVTPGTPIGPDGFGKEGECLEARSFESWTPTNYKQCSWSLNYGIDL 120
DB 61 GVPGRDGSFGANVTPGTPIGPDGFGKEGECLEARSFESWTPTNYKQCSWSLNYGIDL 120
QY 121 GKIAECTFTKRSNSALRYLFGSGLRLKCRNACCQRYWTFPGAECGSPLEAIITVYDQ 180
DB 121 GKIAECTFTKRSNSALRYLFGSGLRLKCRNACCQRYWTFPGAECGSPLEAIITVYDQ 180
QY 181 GSPENNSTINIRHTSSVEGLCEGIGAGLVDAIHWGTCSDYKDGASTGMSVSRIITIEE 240
DB 181 GSPENNSTINIRHTSSVEGLCEGIGAGLVDAIHWGTCSDYKDGASTGMSVSRIITIEE 240
QY 241 LPK 243
DB 241 LPK 243

RESULT 12

US-10-175-737-366
; Sequence 366, Application US/10175737
; Publication No. US20030013153A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Auecin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C50
; CURRENT APPLICATION NUMBER: US/10/175,737
; PRIOR APPLICATION DATE: 2002-06-19
; PRIOR APPLICATION REMOVED - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 366
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-737-366

PRIOR APPLICATION NUMBER: 60/077649
 PRIOR FILING DATE: 1998-03-11
 PRIOR APPLICATION NUMBER: 60/078886
 PRIOR FILING DATE: 1998-03-20
 PRIOR APPLICATION NUMBER: 60/078939
 PRIOR FILING DATE: 1998-03-20
 PRIOR APPLICATION NUMBER: 60/079664
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/079786
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/080107
 PRIOR FILING DATE: 1998-03-31
 PRIOR APPLICATION NUMBER: 60/080194
 PRIOR FILING DATE: 1998-03-31
 PRIOR APPLICATION NUMBER: 60/080327
 PRIOR FILING DATE: 1998-04-01
 PRIOR APPLICATION NUMBER: 60/080333
 PRIOR FILING DATE: 1998-04-01
 PRIOR APPLICATION NUMBER: 60/081049
 PRIOR FILING DATE: 1998-04-08
 PRIOR APPLICATION NUMBER: 60/081070
 PRIOR FILING DATE: 1998-04-08
 PRIOR APPLICATION NUMBER: 60/081195
 PRIOR FILING DATE: 1998-04-09
 PRIOR APPLICATION NUMBER: 60/081838
 PRIOR FILING DATE: 1998-04-15
 PRIOR APPLICATION NUMBER: 60/082568
 PRIOR FILING DATE: 1998-04-21
 PRIOR APPLICATION NUMBER: 60/082569
 PRIOR FILING DATE: 1998-04-21
 PRIOR APPLICATION NUMBER: 60/082704
 PRIOR FILING DATE: 1998-04-22
 PRIOR APPLICATION NUMBER: 60/082797
 PRIOR FILING DATE: 1998-04-22
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 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083559
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/084366
 PRIOR FILING DATE: 1998-05-05
 PRIOR APPLICATION NUMBER: 60/084414
 PRIOR FILING DATE: 1998-05-06
 PRIOR APPLICATION NUMBER: 60/084639
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 PRIOR APPLICATION NUMBER: 60/086023
 PRIOR FILING DATE: 1998-05-18
 PRIOR APPLICATION NUMBER: 60/086392
 PRIOR FILING DATE: 1998-05-22
 PRIOR APPLICATION NUMBER: 60/086486
 PRIOR FILING DATE: 1998-05-22
 PRIOR APPLICATION NUMBER: 60/087098
 PRIOR FILING DATE: 1998-05-28
 PRIOR APPLICATION NUMBER: 60/087208

PRIOR FILING DATE: 1998-05-28
 PRIOR APPLICATION NUMBER: 60/087609
 PRIOR FILING DATE: 1998-06-02
 PRIOR APPLICATION NUMBER: 60/087759
 PRIOR FILING DATE: 1998-06-02
 PRIOR APPLICATION NUMBER: 60/087827
 PRIOR FILING DATE: 1998-06-03
 PRIOR APPLICATION NUMBER: 60/088025
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088028
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088029
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 PRIOR FILING DATE: 1998-06-11
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 PRIOR APPLICATION NUMBER: 60/089105
 PRIOR FILING DATE: 1998-06-12
 PRIOR APPLICATION NUMBER: 60/089512
 PRIOR FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: 60/089514
 PRIOR FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: 60/089538
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089598
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089653

Query Match 100.0%; Score 243; DB 14; Length 243;
 Best Local Similarity 100.0%; Pred. No. 1,8e-211; Indels 0; Gaps 0;
 Matches 243; Conservative 0; Mismatches 0;

QY 1 MRQGPASPOLRLTLLTLLQPPASSASEIPKQKQQLRQREVVDLYNGMCLQGP 60
 DB 1 MRQGPASPOLRLTLLTLLQPPASSASEIPKQKQQLRQREVVDLYNGMCLQGP 60
 QY 61 GVPGRDGSFGANVLPGTPIGPRDGFKEGKECIRSEFSESWTPNKKCSWSLNGIDL 120
 DB 61 GVPGRDGSFGANVLPGTPIGPRDGFKEGKECIRSEFSESWTPNKKCSWSLNGIDL 120

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QY 121 GKIAECTFTKMSNSALRYLFSGSLRLKCRNACCORWYFTFNGAECSGPLPIEAIITYLDQ 180
    |||
DB 121 GKIAECTFTKMSNSALRYLFSGSLRLKCRNACCORWYFTFNGAECSGPLPIEAIITYLDQ 180
QY 181 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIIVWGTCSDYPKGDASTGMNSVSRIIIEE 240
    |||
DB 181 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIIVWGTCSDYPKGDASTGMNSVSRIIIEE 240
QY 241 LPK 243
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DB 241 LPK 243
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RESULT 15

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US-10-176-483-366
; Sequence 366, Application US/10176483
; Publication No. US20030017541A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C68
; CURRENT APPLICATION NUMBER: US/10/176,483
; CURRENT FILING DATE: 2002-06-20
; Prior application removed - See file wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 366
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-483-366
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Query Match 100.0%; Score 243; DB 14; Length 243;
Best Local Similarity 100.0%; Pred. No. 1.8e-211; Indels 0; Gaps 0;
Matches 243; Conservative 0; Mismatches 0;
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QY 1 MRPOGPAASPORLRLGLLLLLQLPAPSSASEIPKQKQAKQLRQREVVDLYNGMCLQGPA 60
    |||
DB 1 MRPOGPAASPORLRLGLLLLLQLPAPSSASEIPKQKQAKQLRQREVVDLYNGMCLQGPA 60
QY 61 GYPGRDGSFGANYIPGTGPIGRDGFKEGKECLRESFEBSWTPNTYKQCSWSSLYNGIDL 120
    |||
DB 61 GYPGRDGSFGANYIPGTGPIGRDGFKEGKECLRESFEBSWTPNTYKQCSWSSLYNGIDL 120
QY 121 GKIAECTFTKMSNSALRYLFSGSLRLKCRNACCORWYFTFNGAECSGPLPIEAIITYLDQ 180
    |||
DB 121 GKIAECTFTKMSNSALRYLFSGSLRLKCRNACCORWYFTFNGAECSGPLPIEAIITYLDQ 180
QY 181 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIIVWGTCSDYPKGDASTGMNSVSRIIIEE 240
    |||
DB 181 GSPENNSTINIHRTSSVEGLCEGIGAGLVDAIIVWGTCSDYPKGDASTGMNSVSRIIIEE 240
QY 241 LPK 243
    |||
DB 241 LPK 243
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Search completed: December 25, 2004, 05:35:09
Job time : 70 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 25, 2004, 05:28:06 ; Search time 23 Seconds
(without alignments)
1016.551 Million cell updates/sec

Title: US-10-063-734-122

Perfect score: 243

Sequence: 1 MKPGPASPSPRLRGILLLL.....GDASTGMNSVSRRIIEBLPK 243

Scoring table: <OLIGO>

Gapop 60.0 , Gapept 60.0

Searched: 283416 seqs, 96216763 residues

Word size: 6

Total number of hits satisfying chosen parameters: 1982

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9	3.7	133	2	S57038
2	9	3.7	144	2	T18867
3	9	3.7	247	2	A55717
4	9	3.7	779	1	CG801S
5	9	3.7	996	2	JB0237
6	9	3.7	1464	1	CGHUIS
7	8	3.3	112	2	AG0111
8	8	3.3	141	1	UTRUB
9	8	3.3	165	1	KITHUB
10	8	3.3	169	2	T18321
11	8	3.3	177	2	S37749
12	8	3.3	249	2	T35724
13	8	3.3	254	2	I38427
14	8	3.3	291	2	B60131
15	8	3.3	296	2	T24827
16	8	3.3	302	2	T21257
17	8	3.3	307	2	S36779
18	8	3.3	330	2	S46657
19	8	3.3	333	2	T20436
20	8	3.3	360	2	T37285
21	8	3.3	365	2	UC7694
22	8	3.3	368	2	AE0086
23	8	3.3	378	2	T00481
24	8	3.3	391	2	D72663
25	8	3.3	399	2	CB3611
26	8	3.3	424	2	C70371
27	8	3.3	457	1	RMWST4
28	8	3.3	487	1	A26660
29	8	3.3	487	2	S54785

30	8	3.3	500	2	S66522	cartilage matrix p
31	8	3.3	636	2	S41067	collagen alpha 1(I)
32	8	3.3	674	2	S23297	collagen alpha 1(X)
33	8	3.3	809	2	A45747	Na+/H+-exchanging
34	8	3.3	917	2	S09646	collagen alpha 2(V)
35	8	3.3	984	2	S67527	protein kinase (EC
36	8	3.3	1018	1	CGH02A	collagen alpha 2(V)
37	8	3.3	1029	1	S21369	collagen alpha 1(X)
38	8	3.3	1102	2	JH0717	guanylate cyclase
39	8	3.3	1108	2	A55915	guanylate cyclase
40	8	3.3	1120	2	H88449	protein F54D8.1 (I)
41	8	3.3	1265	1	A37967	neural cell adhesi
42	8	3.3	1278	2	T30188	Niemann-Pick C dis
43	8	3.3	1388	2	A53317	collagen alpha 1(X)
44	8	3.3	1414	1	S23809	collagen alpha 2(I)
45	8	3.3	1433	2	A46053	bullous pemphigoid

ALIGNMENTS

RESULT 1
S57038
probable membrane protein YJR023c - Yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein J1470; hypothetical protein YJR83.19
C:Species: Saccharomyces cerevisiae
C>Date: 08-Jul-1995 #sequence_revision 08-Sep-1995 #text_change 03-Jul-2004
C/Accession: S57038; S57041; S55212
R:de Haan, M.; Grivell, L.A.; Smits, P.H.M.
submitted to the Protein Sequence Database, September 1995
A:Reference number: S56771
A:Accession: S57038
A:Molecule type: DNA
A:Residues: 1-133 <ZAG>
A:Cross-references: UNIPROT:P47094; EMBL:249522; NID:g1015659; PID:g1015661
R:Zagalski, M.; Babinska, B.; Gromacka, R.; Migdalski, A.; Rytka, J.; Sulicka, J.; Herber
submitted to the Protein Sequence Database, September 1995
A:Reference number: S57040
A:Accession: S57041
A:Molecule type: DNA
A:Residues: 1-93 <HDA>
A:Cross-references: EMBL:249522; MIPS:YJR023c
R:de Haan, M.; Smits, P.H.M.; Grivell, L.A.
submitted to the EMBL Data Library, May 1995
A:Reference number: S55183
A:Accession: S55212
A:Molecule type: DNA
A:Residues: 1-133 <DEH>
A:Cross-references: EMBL:X87611
C:Genetics:
A:Cross-references: SGD:S0003784
A:Map position: 10R
C:Superfamily: Saccharomyces probable membrane protein YJR023c
C:Keywords: transmembrane protein

Query Match 3.7%; Score 9; DB 2; Length 133;
Best Local Similarity 100.0%; Pred. No. 0.56;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 LLLLLLQL 24
DB 22 LLLLLLQL 30

RESULT 2
T18867
hypothetical protein CO2F4.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T18867
R:Cummings, P.
submitted to the EMBL Data Library, October 1996
A:Reference number: Z19034

Db 586 PGRDSCPGA 594

RESULT 5

JE0237

apolipoprotein E receptor 2 precursor - mouse

N:Alternate names: apoB2

C:Species: Mus musculus (house mouse)

C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 09-Jul-2004

C:Accession: JE0237

R:Kim, H.J.; Kim, D.H.; Magoori, K.; Saeki, S.; Yamamoto, T.T.

J. Biochem. 124, 451-456, 1998

A:Title: Evolution of the apolipoprotein E receptor 2 gene by exon loss.

A:Reference number: JE0237; MUID:98352008; PMID:9685741

A:Accession: JE0237

A:Molecule type: mRNA

A:Residues: 1-996 <TIM>

C:Superfamily: LDL receptor; EGF homology; LDL receptor ligand-binding repeat homology;

C:Keywords: glycoprotein

F:1-35/Domain: signal sequence #status predicted <SIG>

F:36-996/Product: apolipoprotein E receptor 2 #status predicted <MAT>

F:41-75/Domain: LDL receptor ligand-binding repeat homology <LDL1>

F:80-116/Domain: LDL receptor ligand-binding repeat homology <LDL2>

F:121-157/Domain: LDL receptor ligand-binding repeat homology <LDL3>

F:161-195/Domain: LDL receptor ligand-binding repeat homology <LDL4>

F:200-237/Domain: LDL receptor ligand-binding repeat homology <LDL5>

F:251-286/Domain: LDL receptor ligand-binding repeat homology <LDL6>

F:291-325/Domain: LDL receptor ligand-binding repeat homology <LDL7>

F:331-368/Domain: LDL receptor ligand-binding repeat homology <LDL8>

F:372-407/Domain: EGF homology <EGF>

F:585-628/Domain: LDL receptor WTD-containing repeat homology <WTV>

F:782-767/Domain: EGF homology <EGF1>

F:858-881/Domain: transmembrane #status predicted <TM>

F:805,840/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 3.7%; Score 9; DB 2; Length 996;

Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LLLLLLQL 24

Db 14 LLLLLLQL 22

RESULT 6

CGHUS

collagen alpha 1(I) chain precursor - human

N:Alternate names: procollagen alpha 1(I) chain

C:Species: Homo sapiens (man)

C:Date: 12-Aug-1981 #sequence_revision 04-Oct-1996 #text_change 09-Jul-2004

C:Accession: I60114; S01143; A33335; I55254; A39943; I55237; A35233; S09400; B90567; S11569; A29439; I55466; A02852; I37247

R:D'Alessio, M.; Bernard, M.; Pretorius, P.J.; de Wet, W.; Ramirez, F.; Pretorius, P.J.

Gene 67, 105-115, 1988

A:Title: Complete nucleotide sequence of the region encompassing the first twenty-five e

A:Reference number: I60114; MUID:88329734; PMID:2843432

A:Accession: I60114

A:Status: translated from GB/EMBL/DBD

A:Molecule type: DNA

A:Residues: 1-369, 'V', 371-589 <DAL>

A:Cross-references: UNIPROT: P02452; UNIPROT: Q14992; UNIPROT: Q16053; UNIPROT: Q13896; UNITH

R:Chou, G.; Kuvshinov, H.; Stacey, A.; Shikata, H.; Baldwin, C.T.; Jaenisch, R.; Brock

Biochem. J. 253, 919-922, 1988

A:Title: Structure of a full-length cDNA clone for the prepro-alpha-1(I) chain of human

A:Reference number: S01143; MUID:89025644; PMID:3178743

A:Accession: S01143

A:Molecule type: mRNA

A:Residues: 1-472 <TRO>

A:Cross-references: EMBL: X07884; NID: G30015; PID: CA30731.1; PID: G30016; GB: M3546; NIT

R:Chu, M.L.; de Wet, W.; Bernard, M.; Ding, J.F.; Morabito, M.; Myers, J.; Williams, C.

Nature 310, 337-340, 1984

A:Title: Human procollagen(I) collagen gene structure reveals evolutionary conservation of
A:Reference number: A93335; PMID:84270697; PMID:6462220
A:Accession: A93335
A:Molecule type: DNA
A:Residues: 1-58, 'Q', 60-181 <CHD>
A:Cross-references: EMBL:X00820; NID:935657; PIDN:CAA25394.1; PID:935658
R:Rosnow, C.M.S.; Vengoe, W.P.; du Plooy, S.J.; Bernard, M.P.; Ramirez, F.; de Wet, W.
J. Biol. Chem. 262, 15151-15157, 1987
A:Title: DNA sequences in the first intron of the human pro-alpha 1(I) collagen gene enhi
A:Reference number: 155254; PMID:88033098; PMID:2822714
A:Accession: 155254
A:Status: translation not shown; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-45 <ROS>
A:Cross-references: GB:J02829; NID:9180387; PIDN:AA51993.1; PID:9180388
R:Bornstein, P.; McKay, J.; Morishima, J.K.; Devaryayalu, S.; Gellinas, R.E.
Proc. Natl. Acad. Sci. U.S.A. 84, 8869-8873, 1987
A:Title: Regulatory elements in the first intron contribute to transcriptional control of
A:Reference number: A39943; PMID:88097389; PMID:3480516
A:Accession: A39943
A:Molecule type: DNA
A:Residues: 1-34 <BOR>
A:Cross-references: GB:J03559; NID:9180876; PIDN:AA52052.1; PID:9553238
R:Chu, M.L.; de Wet, W.; Bernard, M.; Ramirez, F.
J. Biol. Chem. 260, 2315-2320, 1985
A:Title: Fine structural analysis of the human pro-alpha 1 (I) collagen gene. Promoter st
A:Reference number: 155237; PMID:85130970; PMID:2857713
A:Accession: 155237
A:Status: translation not shown; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-34 <CHD>
A:Cross-references: GB:M10627; NID:9180383; PIDN:AA51992.1; PID:9553226
R:Witz, M.K.; Keene, D.R.; Horv, H.; Glanville, R.W.; Steinhann, B.; Rao, V.H.; Hollist
J. Biol. Chem. 265, 6312-6317, 1990
A:Title: In vivo and in vitro noncovalent association of excised alpha1(I) amino-terminal
rom, type VII
A:Reference number: A35233; PMID:90202908; PMID:2318855
A:Accession: A35233
A:Molecule type: protein
A:Residues: 33-52 <MIR>
A:Note: this propeptide fragment remained non-covalently bound to a defective, uncleaved
R:Well, D.; d'Alessio, M.; Ramirez, F.; de Wet, W.; Cole, W.G.; Chan, D.; Bateman, J.F.
EMBO J. 8, 1705-1710, 1989
A:Title: A base substitution in the exon of a collagen gene causes alternative splicing
A:Reference number: S09400; PMID:89356643; PMID:2767050
A:Accession: S09400
A:Molecule type: mRNA
A:Residues: 156-183 <MEI>
R:Click, E.M.; Bornstein, P.
Biochemistry 9, 4699-4706, 1970
A:Title: Isolation and characterization of the cyanogen bromide peptides from the alpha1
A:Reference number: A90567; PMID:71038655; PMID:5529814
A:Contents: CNBR0-1, CNBR2, CNBR4, CNBR5
A:Accession: B90567
A:Molecule type: protein
A:Residues: 162-199, 'Z', 200-201, 'Z', 203-206, 'Z', 208-209, 'Z', 211-228, 'B', 230, 'BB', 233, 'Z',
A:Experimental source: skin
A:Note: evidence for 170-alysine
R:Baetge, B.; Notbhm, H.; Diebold, J.; Lehmann, H.; Bodo, M.; Deutzmann, R.; Mueller, P
Eur. J. Biochem. 192, 153-159, 1990
A:Title: A critical crosslink region in human-bone-derived collagen type I. Specific clea
A:Reference number: 511372; PMID:90382436; PMID:2169412
A:Accession: 511372
A:Molecule type: protein
A:Residues: 175-187, 274-287, 'P', 289 <BAE>
A:Note: sequence of collagen alpha 1(S)(I) isolated from bone after pepsin digestion
R:Deak, S.B.; Scholtz, P.M.; Amenta, P.S.; Constantinou, C.D.; Levi-Minzi, S.A.; Gonzalez
J. Biol. Chem. 266, 21827-21832, 1991
A:Title: The substitution of arginine for glycine 85 of the alpha 1(I) procollagen chain
operative melting of intact type I collagen.
A:Reference number: 155342; PMID:92042092; PMID:1718984
A:Accession: 155342
A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA
A:Residues: 258-268/1347-1357 <DEA>
A:Cross-references: GB:S67495; NID:9239007; PIDN:AA20350.1; PID:9239008
A>Note: sequences from the 5' and 3' ends only are shown; mutant sequence 263-Arg report
R:Morgan, P.H.; Jacobs, H.G.; Segre, J.P.; Cunningham, L.W.
J. Biol. Chem. 245, 5042-5048, 1970
A:Title: Comparative study of glycopeptides derived from selected vertebrate collagens.
A:Reference number: A92069; MUID:71001508; PMID:4319110
A:Accession: A92069
A:Molecule type: protein
A:Residues: 263-268 <MOR>
A:Experimental source: skin
A>Note: attachment of 2-O-alpha-D-glucosyl-O-beta-D-galactose to 5-hydroxylysine
R:Labhad, M.E.; Hollister, D.W.
Matrix 10, 124-130, 1990
A:Title: Segmental amplification of the entire helical and telopeptide regions of the CT
A:Reference number: S15989; MUID:90326017; PMID:2374517
A:Accession: S15989
A:Molecule type: mRNA
A:Residues: 281-302/402-420/823-843/925-944/1026-1045/1143-1162 <LAB>
R:Wirtz, M.K.; Rao, V.H.; Glanville, R.W.; Labhad, M.E.; Pretorius, P.J.; de Vries, W.N.
Connect. Tissue Res. 29, 1-11, 1993
A:Title: A cysteine for glycine substitution at position 175 in an alpha 1 (I) chain of
A:Reference number: 152905; MUID:93339042; PMID:8339541
A:Accession: 152905
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 342-352, 'C', 354-359 <W12>
A:Cross-references: GB:S64717; NID:9408195; PIDN:AA27677.1; PID:9408196
A>Note: mutant sequence from patient with osteogenesis imperfecta
R:Bernard, M.P.; Chu, M.L.; Myers, J.C.; Ramirez, F.; Elenderry, E.F.; Prockop, D.J.
Biochemistry 22, 5213-5223, 1983
A:Title: Nucleotide sequences of complementary deoxyribonucleic acids for the proalpha1
A:Reference number: A90476; MUID:84080385; PMID:6689127
A:Accession: A90476
A:Molecule type: mRNA
A:Residues: 425-1250, 'X', 1252-1328, 'S', 1330-1390, 'X', 1397-1464 <BER>
A:Cross-references: GB:K01228; NID:9180391; PIDN:AA51847.1; PID:9180392
A>Note: sequence partially completed for missing nucleotides by A93439
R:Chu, M.L.; Gargiulo, V.; Williams, C.O.; Ramirez, F.
J. Biol. Chem. 260, 691-694, 1985
A:Title: Multielectron deletion in an osteogenesis imperfecta variant with increased type II
A:Reference number: A22161; MUID:85104934; PMID:2981843
A:Accession: A22161
A:Molecule type: DNA
A:Residues: 472-594, 'R', 596-607 <CH3>
A:Cross-references: GB:K03178; GB:K03179; NID:9179612; NID:9179613; PIDN:AA51847.1; PID
R:Wallis, G.A.; Starman, B.J.; Zimm, A.B.; Byers, P.H.
Am. J. Hum. Genet. 46, 1034-1040, 1990
A:Title: Variable expression of osteogenesis imperfecta in a nuclear family is explained
A:Reference number: A35336; MUID:90252792; PMID:2339700
A:Accession: A35336
A:Molecule type: mRNA
A:Residues: 710-720, 'E', 722-737, 'E', 739-745 <WAL>
A>Note: the authors translated the codons CAG for 721 and CGT for 738 as Glu
R:Forlino, A.; Zollezzi, F.; Valli, M.; Pignatti, P.F.; Cetta, G.; Brunelli, P.C.; Mottes
Hum. Mol. Genet. 3, 2201-2206, 1994
A:Title: Severe (type III) osteogenesis imperfecta due to glycine substitutions in the C
A:Reference number: 154355; MUID:95187161; PMID:7881420
A:Accession: 154355
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 746-766, 'S', 768-781 <FOR>
A:Cross-references: GB:L47667; NID:91009093; PIDN:AA55576.1; PID:91009094
R:Chesler, S.D.; Wallis, G.A.; Byers, P.H.
J. Biol. Chem. 268, 18218-18225, 1993
A:Title: Mutations in the carboxyl-terminal propeptide of the pro alpha 1(I) chain of ty
A:Reference number: A47426; MUID:93352646; PMID:8349697
A:Accession: A47426
A:Molecule type: mRNA
A:Residues: 1179-1276, 'H', 1278-1336, 1339-1387, 'R', 1389-1464 <CHE>

A:Cross-references: GB:S64596; NID:9407589; PIDN:AA27856.1; PID:9407590
A>Note: sequence extracted from NCBI backbone (NCBI:136444, NCBI:136445)
A>Note: does not represent an experimentally determined sequence but three different mut
A:Accession: B47426
A:Molecule type: mRNA
A:Residues: 1179-1464 <CH4>
A:Experimental source: normal dermal fibroblast culture
A:Accession: C47426
A:Molecule type: mRNA
A:Residues: 1179-1276, 'H', 1278-1464 <CH5>
A:Experimental source: fetal cell 86-237
A:Accession: D47426
A:Molecule type: mRNA
A:Residues: 1179-1336, 1339-1464 <CH6>
A:Experimental source: fetal cell 86-146
A:Accession: E47426
A:Molecule type: mRNA
A:Residues: 1179-1387, 'R', 1389-1464 <CH7>
A:Experimental source: fetal cell 88-251
R:Chen, D.H.; Apone, S.; Eyre, D.R.; Starman, B.J.; Andreassen, P.; Charbonneau, H.; Nicl
J. Biol. Chem. 263, 14605-14607, 1988
A:Title: Substitution of Cysteine for Glycine within the Carboxyl-terminal Telopeptide of
A:Reference number: 155269; MUID:89008319; PMID:3170557
A:Accession: 155269
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1187-1194, 'C', 1196-1220 <COH>
A:Cross-references: GB:M23213; NID:9340842; PIDN:AA59363.1; PID:9499622
A>Note: mutant sequence from a patient with mild osteogenesis imperfecta
R:Maekelae, J.K.; Raasina, M.; Virta, A.; Vuorio, E.
Nucleic Acids Res. 16, 349, 1988
A:Title: Human pro-alpha-1(I) collagen: cDNA sequence for the C-propeptide domain.

Query Match 3.7%; Score 9; DB 1; Length 1464;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 63 PGRDGPQA 71
DB 1024 PGRDGPQA 1032

RESULT 7
A60111
sporozoite antigen - Elmeria tenella (fragment)
C:Species: Elmeria tenella
C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 17-Jul-1994
C:Accession: A60111
R:Miller, G.A.; Bhogal, B.S.; McCandlish, R.; Strauberg, R.L.; Jessee, E.J.; Anderson, J
Infect. Immun. 57, 2014-2020, 1989
A:Title: Characterization and vaccine potential of a novel recombinant coccidial antigen.
A:Reference number: A60111; MUID:89277516; PMID:2659532
A:Accession: A60111
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-112 <MIL>

Query Match 3.3%; Score 8; DB 2; Length 112;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 LLLLLLQ 23
DB 3 LLLLLLQ 10

RESULT 8
UTRUB
luteoprotein beta chain precursor [validated] - human
N:Alternate names: interstitial cell-stimulating hormone (ICSH) beta chain; luteinizing h
C:Species: Homo sapiens (man)
C:Date: 13-Jul-1981 #sequence_revision 24-Nov-1999 #text_change 09-Jul-2004
C:Accession: I37994; I58013; A90604; A92759; A94466; A01497; B94552

R:Palma, K.; Vamvakopoulos, N.C.; Fidler, J.C.
 Nature 307, 37-40, 1984
 A:Title: Evolution of the genes for the beta subunits of human chorionic gonadotropin and
 A:Reference number: I37231; MUID:84093550; PMID:669082
 A:Accession: I37994
 A:Status: preliminary; translated from GB/EMBL/DBJ; not compared with conceptual transla
 A:Molecule type: DNA
 A:Residues: 1-141 <PAL>
 A:Cross-references: UNIPROT:P01229; GB:X00264; NID:g34351; PIDN:CAA25067.1; PID:g2292893
 R:Weiss, J.; Axelrod, L.; Whitcomb, R.W.; Harris, P.E.; Crowley, W.F.; Jamieson, J.L.
 N. Engl. J. Med. 326, 179-183, 1992
 A:Title: Hypogonadism caused by a single amino acid substitution in the beta subunit of
 A:Reference number: I58013; MUID:92085985; PMID:127547
 A:Accession: I58013
 A:Status: translation not shown; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 72-73, 'R', 75-76 <WEI>
 A:Cross-references: GB:S71273; NID:g40572; PIDN:AAD14960.1; PID:g4262812
 A:Note: mutant sequence from patient with hypogonadism
 R:Saltram, M.R.; Li, C.H.
 Biochim. Biophys. Acta 412, 70-81, 1975
 A:Title: Human pituitary luteotropin. Isolation, properties, and the complete amino acid se
 A:Reference number: A90604; MUID:76062547; PMID:1191677
 A:Accession: A90604
 A:Molecule type: protein
 R:Shome, B.; Parlow, A.F.
 J. Clin. Endocrinol. Metab. 36, 618-621, 1973
 A:Title: The primary structure of the hormone-specific, beta subunit of human pituitary
 A:Reference number: A92759; MUID:73090987; PMID:4685398
 A:Accession: A92759
 A:Molecule type: protein
 A:Residues: 21-38, 'Q', 40-75, 77-131, 133-134, 'H', 136-137 <SHO>
 R:Cloisset, J.; Hennen, G.; Leguin, R.M.
 FEBS Lett. 29, 97-100, 1973
 A:Title: Human luteinizing hormone the amino acid sequence of the beta subunit.
 A:Reference number: A91389; MUID:73221227; PMID:4719207
 A:Contents: annotation; partial sequence
 R:Ward, D.N.
 unpublished results, cited by Cloisset, J., Hennen, G., and Leguin, R.M., FEBS Lett. 29,
 A:Reference number: A94466
 A:Accession: A94466
 A:Molecule type: protein
 A:Residues: 21-38, 'Q', 40-46 <WAB>
 A:Note: 28-Val, 33-Arg, and 35-Thr were also found
 R:Shome, B.; Parlow, A.F.
 submitted to the Atlas, April 1975
 A:Reference number: A94552
 A:Contents: annotation; binding site
 C:Genetics:
 A:Gene: GDB:LHB
 A:Cross-references: GDB:119364; OMIM:152780
 A:Map position: 19q13.3-19q13.3
 C:Superfamily: pituitary glycoprotein hormone beta chain
 C:Keywords: blocked amino end; glycoprotein; hormone; pituitary
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-141/Product: luteotropin beta #status predicted <LIT>
 F:1/Modified site: blocked amino end (Ser) (in mature form) (probably acetylated) #stat
 F:29-54, 43-77, 46-108, 58-130, 92-130, 110-113/Disulfide bonds: #status predicted
 F:50/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 3.3%; Score 8; DB 1; Length 141;
 Best Local Similarity 100.0%; Pred.No.5.3;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 GULLLLLL 22
 |||||
 Db 6 GULLLLLL 13

RESULT 9
 KTRUB
 choriongonadotropin beta chain precursor [validated] - human

N:Alternate names: beta-gonadotropin; chorionic gonadotropin beta chain
 C:Species: Homo sapiens (man)
 C>Date: 23-Oct-1981 #sequence revision 23-Oct-1981 #text change 09-Jul-2004
 C:Accession: A92230; 169972; I55224; I55250; I70007; I70008; A92303; A92181; A92142; PC1
 R:Fidder, J.C.; Goodman, H.M.
 Nature 286, 684-687, 1980
 A:Title: The cDNA for the beta-subunit of human chorionic gonadotropin suggests evolution
 A:Reference number: A92230; MUID:81012134; PMID:674259
 A:Accession: A92230
 A:Molecule type: mRNA
 A:Residues: 1-165 <FID>
 A:Cross-references: UNIPROT:P01233; GB:J00117; GB:M38559; GB:M54963; NID:g180436; PIDN:A
 R:Policaastro, P.; Ovit, C.E.; Hoshina, M.; Fukuoaka, H.; Boothby, M.R.; Boime, I.
 J. Biol. Chem. 258, 11492-11499, 1983
 A:Title: The beta subunit of human chorionic gonadotropin is encoded by multiple genes.
 A:Reference number: I55224; MUID:84008141; PMID:6194155
 A:Accession: I69972
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-165 <POL>
 A:Cross-references: GB:K03189; NID:g180450; PIDN:AAA53288.1; PID:g180453
 A:Note: clone CG-beta-e
 A:Accession: I55224
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-23, 'M', 25-136, 'A', 138-165 <PO2>
 A:Cross-references: GB:K03183; NID:g180442; PIDN:AAA53287.1; PID:g180444
 A:Note: clone CG-beta-a
 R:Policaastro, P.F.; Daniels-McQueen, S.; Carle, G.; Boime, I.
 J. Biol. Chem. 261, 5907-5916, 1986
 A:Title: A map of the hCG beta-LH beta gene cluster.
 A:Reference number: I55250; MUID:86195987; PMID:2422163
 A:Accession: I55250
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-5 <PO3>
 A:Cross-references: GB:M13504; NID:g180419; PIDN:AAA52005.1; PID:g463088
 A:Note: CG-beta-3 gene
 A:Accession: I70007
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-5 <PO4>
 A:Cross-references: GB:M13505; NID:g180429; PIDN:AAA52008.1; PID:g463089
 A:Note: CG-beta-6 gene
 A:Accession: I70008
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-5 <RES>
 A:Cross-references: GB:M13503; NID:g180432; PIDN:AAA52009.1; PID:g463090
 A:Note: CG-beta-7 gene
 R:Birken, S.; Fetherston, J.; Canfield, R.; Boime, I.
 J. Biol. Chem. 256, 1816-1823, 1981
 A:Title: The amino acid sequences of the prepeptides contained in the alpha and beta sub
 A:Reference number: A92303; MUID:81117268; PMID:7462224
 A:Accession: A92303
 A:Molecule type: protein
 A:Residues: 1-20 <BIR>
 A:Note: the identity of the residue at position 19 could not be determined
 R:Morgan, F.J.; Birken, S.; Canfield, R.E.
 J. Biol. Chem. 250, 5247-5258, 1975
 A:Title: The amino acid sequence of human chorionic gonadotropin. The alpha subunit and t
 A:Reference number: A92181; MUID:75211304; PMID:1150658
 A:Accession: A92181
 A:Molecule type: protein
 A:Residues: 21-165 <MOR>
 R:Carlsen, R.B.; Bahl, O.P.; Swaminathan, N.
 J. Biol. Chem. 248, 6810-6827, 1973
 A:Reference number: A92142; MUID:74011267; PMID:4795659
 A:Accession: A92142
 A:Molecule type: protein
 A:Residues: 21-22, 'Q', 24-73, 'ZL', 76-140, 142-157, 'PB', 160-165, 'SLP', <CAR>
 R:Shi, Z.P.; Du, G.G.; Li, W.X.; Liu, X.J.; Li, S.Z.; Xu, Y.S.; Wang, Y.
 Chinese Biochem. J. 6, 558-562, 1990

A>Title: The immunological characteristics of the enzymatic fragments of human chorionic
 A/Reference number: PCI016
 A/Accession: PCI016
 A/Molecule type: protein
 A/Residues: 21-165 <SHT>
 A/Note: article in Chinese with English abstract
 R/Birken, S.; Armstrong, B.G.; Kolke, M.A.G.; Cole, L.A.; Agosto, G.M.; Krichevsky, A.;
 Endocrinology 123, 572-583, 1988
 A/Title: Structure of the human chorionic gonadotropin beta-subunit fragment from pregna
 A/Reference number: A61097; MUID:88254680; PMID:2454811
 A/Accession: A61097
 A/Molecule type: protein
 A/Residues: 26-32,'X',34-49,'X',51-60,75-112 <B12>
 A/Note: this material from pregnancy urine lacks sialic acid in its carbohydrate and has
 R/Kardana, A.; Bagshaw, K.D.; Cole, B.; Read, D.; Taylor, M.
 A/Title: Characterisation of UGP and its relationship with beta-core fragment.
 A/Reference number: A56873; MUID:93229246; PMID:8471426
 A/Accession: B56873
 A/Molecule type: protein
 A/Residues: 26-28,'X',30-32,'X',34-42,'X',44-45,'X',47-48,75-76,'X',78-91,'G',93-102 <K
 A/Experimental source: urine
 A/Note: sequence modified after extraction from NCBI backbone
 A/Note: this material was designated urinary gonadotropin peptide (peak 2)
 R/Lapthorn, A.J.; Harris, D.C.; Littlejohn, A.; Luebader, J.W.; Canfield, R.E.; Machin,
 Nature 369, 455-461, 1994
 A/Title: Crystal structure of human chorionic gonadotropin.
 A/Reference number: A44674; MUID:94261179; PMID:8202136
 R/Talmadge, K.; Vamvakopoulos, N.C.; Fiddes, J.C.
 Nature 307, 37-40, 1984
 A/Title: Evolution of the genes for the beta subunits of human chorionic gonadotropin ar
 A/Reference number: I37231; MUID:84093590; PMID:6650962
 A/Accession: I37412
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 21-165 <RES>
 A/Cross-references: EMBL:X00265; NID:G31719; PIDN:CAA25068.1; PID:G1335075
 C/Genetics:
 A/Gene: GDB:CGB
 A/Cross-references: GDB:119055; OMIM:118860
 A/Map position: 19q13.3-19q13.3
 A/Introns: 5/3; 61/3
 A/Note: the choriongonadotropin beta chain locus contains six genes (or pseudogenes)
 C/Superfamily: pituitary glycoprotein hormone beta chain
 C/Keywords: glycoprotein; hormone; pituitary
 F:1-20/Domain: signal sequence #status experimental <SIG>
 F:21-165/Product: choriongonadotropin beta chain #status experimental <MAT>
 F:29-77,43-92,46-110,54-108,58-110,113-120/Disulfide bonds: #status experimental
 F:33-50/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F:136-150/Binding site: carbohydrate (Ser) (covalent) #status predicted
 F:141,147,152,158/Binding site: carbohydrate (Ser) (covalent) #status experimental

Query Match 3.3% Score 8; DB 1; Length 165;
 Best Local Similarity 100.0%; Pred. No. 6.1;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 GILLALL 22
 Db 6 GILLALL 13

RESULT 10
 T18321
 hypothetical protein L7610.12 - Leishmania major
 C/Species: Leishmania major
 C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2002
 C/Accession: T18321
 R/Oliver, K.; Murphy, L.; O'Neill, M.; Lawson, D.; Harris, D.; Rajandream, M.; Ivens, A.;
 submitted to the EMBL Data Library, May 1999
 A/Reference number: Z18876
 A/Accession: T18321
 A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA
 A/Residues: 1-169 <OLI>
 A/Cross-references: EMBL:AL034356; NID:el371878; PIDN:CAA2247.1
 C/Genetics:
 A/Note: L7610.12

Query Match 3.3% Score 8; DB 2; Length 169;
 Best Local Similarity 100.0%; Pred. No. 6.2;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PASPQRL 13
 Db 18 PASPQRL 25

RESULT 11
 S37749
 collagen alpha 2(XIV) chain - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
 C/Accession: S37749
 R/Brown, J.C.; Goldik, R.; Mann, K.; Timpl, R.
 submitted to the EMBL Data Library, October 1993
 A/Description: Structure and stability of the triple helical domains of human collagen XI
 A/Reference number: S37749
 A/Accession: S37749
 A/Molecule type: protein
 A/Residues: 1-177 <BRO>
 A/Cross-references: UNIPROT:Q9UNP6
 C/Comment: Prolines and lysines at the third position of the tripeptide repeating unit (C
 ed and subsequently O-glycosylated.
 C/Genetics:
 A/Gene: COL14A2
 C/Complex: type XIV collagen may be a heterotrimer of alpha 1(XIV) chains and one alpha 1;
 C/Function:
 A/Description: structural component of extracellular matrix: glycoprotein; hydroxylysine; hydroxyprolin
 C/Keywords: coll; extracellular matrix; glycoprotein; hydroxylysine; hydroxyprolin
 F:9,24,39,45,59,62,74,80,86,92,98,106,109,116,119,122,137,140/Modified site: 4-hydroxypr
 F:12/Modified site: 4-hydroxyproline (Pro) (partial) #status experimental
 F:18,143/Modified site: 5-hydroxylysine (Lys) (partial) #status experimental
 F:18,27,143/Binding site: carbohydrate (Lys) (covalent) #status experimental
 F:27/Modified site: 5-hydroxylysine (Lys) (partial) #status experimental

Query Match 3.3% Score 8; DB 2; Length 177;
 Best Local Similarity 100.0%; Pred. No. 6.5;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 63 PGRDSPG 70
 Db 86 PGRDSPG 93

RESULT 12
 T35724
 cobalt transport integral membrane protein - Streptomyces coelicolor
 C/Species: Streptomyces coelicolor
 C/Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
 C/Accession: T35724
 R/Murphy, L.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, January 1998
 A/Reference number: Z21548
 A/Accession: T35724
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-249 <MUR>
 A/Cross-references: UNIPROT:O54188; EMBL:AL021411; PIDN:CAA16216.1; GSPDB:GN00070; SCOEDE
 A/Experimental source: strain A3(2)
 C/Genetics:
 A/Gene: cbjQ; SCOEDE:SC7H1.29C
 C/Superfamily: cobalt transport protein Q homolog

Query Match 3.3% Score 8; DB 2; Length 249;
 Best Local Similarity 100.0%; Pred. No. 8.7;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 58 GPAGVGR 65
 |||||
 Db 54 GPAGVGR 61

RESULT 13

138427
 4-1BB ligand - human
 C:Species: Homo sapiens (man)
 C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
 C:Accession: I38427
 R:Allderson, M.R.; Smith, C.A.; Tough, T.W.; Davis-Smith, T.; Armistage, R.J.; Falk, B.; R
 Bur, J. Immunol. 24, 2219-2227, 1994
 A:Title: Molecular and biological characterization of human 4-1BB and its ligand.
 A:Reference number: I38426; MID:94374434; PMID:8088337
 A:Accession: I38427
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-254 <RES>
 A:Cross-references: UNIPROT:P41273; EMBL:U03398; NID:G571322; PIDN:AAA53134.1; PID:G5713

Query Match 3.3%; Score 8; DB 2; Length 254;
 Best Local Similarity 100.0%; Pred. No. 8.8;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 GLLLLLL 22
 |||||
 Db 34 GLLLLLL 41

RESULT 14

B60131
 homeotic protein Xhox-7.1' - African clawed frog (fragment)
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 16-Aug-2004
 C:Accession: B60131; S14514
 R:Su, M.W.; Suzuki, H.R.; Solursh, M.; Ramirez, F.
 Development 111, 1179-1187, 1991
 A:Title: Progressively restricted expression of a new homeobox-containing gene during Xe
 A:Reference number: A60131; MID:91347929; PMID:1679007
 A:Accession: B60131
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-9, 'P', 11-291 <SUA>
 A:Cross-references: UNIPROT:P35993; EMBL:X58772
 R:Su, M.W.; Suzuki, R.H.; Solursh, M.; Ramirez, F.
 submitted to the EMBL Data Library, December 1990
 A:Reference number: S14513
 A:Accession: S14514
 A:Molecule type: mRNA
 A:Residues: 1-291 <SUA2>
 A:Cross-references: EMBL:X58772; NID:G64784; PIDN:CAA41573.1; PID:G64785
 C:Superfamily: homeobox homology
 C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
 F:161-217/Domain: homeobox homology <HOK>

Query Match 3.3%; Score 8; DB 2; Length 291;
 Best Local Similarity 100.0%; Pred. No. 9.9;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 LLLLLLLQ 23
 |||||
 Db 6 LLLLLLLQ 13

RESULT 15

T24827
 hypothetical protein T11B7.3 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T24827

R.Gardner, A.
 submitted to the EMBL Data Library, September 1995
 A:Reference number: T24827
 A:Accession: T24827

A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-296 <WIL>
 A:Cross-references: UNIPROT:Q22389; EMBL:Z54237; PIDN:CAA90989.1; GSPDB:GN00022; CESP:T11
 C:Genetic8:
 A:Gene: CESP:T11B7.3
 A:Map position: 4
 A:introns: 45/3; 111/1; 270/1

Query Match 3.3%; Score 8; DB 2; Length 296;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 PGIPGRDG 85
 |||||
 Db 266 PGIPGRDG 273

Search completed: December 25, 2004, 05:33:23
 Job time : 24 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 25, 2004, 05:26:21 ; Search time 95 Seconds
(without alignments)
1471.748 Million cell updates/sec

Title: US-10-063-734-122

Perfect score: 243

Sequence: 1 MRPGPASPQRRLGILL...GDASTGMSVSRRIIEELPK 243

Scoring table: 40HGO
Gapop 60.0 , Gapext 60.0

Searched: 1825181 seqs, 575374646 residues

Word size: 6

Total number of hits satisfying chosen parameters: 11652

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	243	100.0	243	2	06UW91
2	243	100.0	243	2	AA089273
3	170	70.0	243	2	096CG8
4	169	69.5	232	2	081X63
5	111	45.7	245	2	08CG08
6	111	45.7	245	2	09DID6
7	9	3.7	53	2	06H8C6
8	9	3.7	86	2	06IH72
9	9	3.7	86	2	06IHS3
10	9	3.7	96	2	06IOT6
11	9	3.7	105	2	06IG45
12	9	3.7	120	1	G0N2_HUMAN
13	9	3.7	120	2	AAH63162
14	9	3.7	133	1	YJZ3_YEAST
15	9	3.7	144	2	P90741
16	9	3.7	163	2	06ILM0
17	9	3.7	191	2	06ILU4
18	9	3.7	205	1	NS9_CEBCA
19	9	3.7	274	2	08OYU5
20	9	3.7	299	2	06IIF0
21	9	3.7	324	2	07NFG2
22	9	3.7	384	2	07XEC4
23	9	3.7	472	2	06BD07
24	9	3.7	501	2	09AVM0
25	9	3.7	558	2	09ASN8
26	9	3.7	779	1	CA11_BOVIN
27	9	3.7	813	1	CADW_RAT
28	9	3.7	905	1	ATIS_MOUSE
29	9	3.7	996	1	LRP8_MOUSE
30	9	3.7	1069	2	06LAN8
31	9	3.7	1069	2	CA67261

32	9	3.7	1348	2	07PYX1	07PYX1 anopheles g
33	9	3.7	1461	2	076045	076045 homo sapien
34	9	3.7	1464	1	CA11_HUMAN	P02452 homo sapien
35	9	3.7	1464	2	08N473	08N473 homo sapien
36	9	3.7	1464	2	06P912	06P912 xenopus lae
37	9	3.7	1464	2	AAH60753	AAH60753 xenopus t
38	9	3.7	1492	2	06P422	06P422 xenopus t
39	9	3.7	1492	2	AAH63191	AAH63191 xenopus t
40	8	3.3	59	2	08K312	08K312 mus musculu
41	8	3.3	65	2	09JZM3	09JZM3 mus musculu
42	8	3.3	79	2	06K251	06K251 oryza sativ
43	8	3.3	79	2	BAD20061	BAD20061 oryza sat
44	8	3.3	79	2	BAD20107	BAD20107 oryza sat
45	8	3.3	108	2	09D9P8	09D9P8 mus musculu

ALIGNMENTS

RESULT 1	ID	06UW91	PRELIMINARY	PRT	243 AA.
AC	06UW91				
DT	05-JUL-2004	(TREMBlrel. 27, Created)			
DT	05-JUL-2004	(TREMBlrel. 27, Last sequence update)			
DT	05-JUL-2004	(TREMBlrel. 27, Last annotation update)			
DE	CTHRC1				
GN	ORFName=UNQ762;				
OS	Homo sapiens (Human)				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.				
OX	NCBI_Taxid=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=22887296; PubMed=12975309;				
RA	Clark H.F., Gurney A.L., Adaya E., Baker K., Baldwin D., Brush J.,				
RA	Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,				
RA	Raton D., Foster J., Grimaldi C., Gu Q., Haas P.B., Heldens S.,				
RA	Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,				
RA	Lewis L., Liao D., Mark W., Robble E., Sanchez C., Schoenfeld J.,				
RA	Seshagiri S., Simmons L., Singh J., Smith V., Slinson J., Vagts A.,				
RA	Vandlen R., Watanabe C., Wiand D., Woods K., Xie M.H., Yansura D.,				
RA	Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,				
RA	Godowski P.;				
RT	"The secreted protein discovery initiative (SPDI), a large-scale				
RT	effort to identify novel human secreted and transmembrane proteins: a				
RT	Bioinformatics assessment."				
RL	Genome Res. 13:2265-2270 (2003).				
DR	EMBL; AY358914; AA089273.1; -				
DR	InterPro; IPR008161; Clg_helix.				
DR	InterPro; IPR008160; Clg_helix.				
DR	ProDom; PD000007; Clg_helix; 1.				
KW	COLLAGEN.				
SQ	SEQUENCE 243 AA; 26266 MW; BCB49AF4DBC0303BC CRC64;				
Query Match	100.0%; Score 243; DB 2; Length 243;				
Best Local Similarity	100.0%; Pred. No. 1.6e-220; Gaps 0;				
Matches 243; Conservative	0; Mismatches 0; Indels 0; Gaps 0;				
QY	1	MRPGPASPQRRLGILLQLLPAPSSASRIPIKQKQAQLRQREVVLDLNGMCLQGP	60		
DB	1	MRPGPASPQRRLGILLQLLPAPSSASRIPIKQKQAQLRQREVVLDLNGMCLQGP	60		
QY	61	GVPRGDSFGANVITGTGIPGRDQKGEKGLRESEFSESTPYKQCSWSLNYGIDL	120		
DB	61	GVPRGDSFGANVITGTGIPGRDQKGEKGLRESEFSESTPYKQCSWSLNYGIDL	120		
QY	121	GKIACTFTKMSNALSRLTFSGLRLKCRNACQGRWFTFGACSGPLPEATITVLDQ	180		
DB	121	GKIACTFTKMSNALSRLTFSGLRLKCRNACQGRWFTFGACSGPLPEATITVLDQ	180		
QY	181	GSPEMNSTINIRTSVEGLCEGAGLVDAIWWGTSDDPKGDASTGMSVSRRIIEE	240		
DB	181	GSPEMNSTINIRTSVEGLCEGAGLVDAIWWGTSDDPKGDASTGMSVSRRIIEE	240		

Db 181 GSEPMNSTINIRHTSSVEGLCEGIGAGLVDAIWMGTCSDPKGDASTGMSVSRILIEE 240
 Qy 241 LPK 243
 ||||
 Db 241 LPK 243

RESULT 2
 AAQ89273 PRELIMINARY; PRT; 243 AA.

ID AAQ89273
 AC AAQ89273; PRELIMINARY; PRT; 243 AA.
 DT 02-MAR-2004 (TREMBlrel. 27, Created)
 DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
 DE 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
 GN CTRHCL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=12975309;
 RA Clark H.F., Gurely A.L., Abaya E., Baker K., Baldwin D., Brush J.,
 Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
 Batton D., Foster J., Grimaldi C., Gu Q., Hays P.E., Heldens S.,
 Huang L., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
 Lewis L., Liao D., Mark M., Robbie R., Sanchez C., Schoenfeld J.,
 Seshadri S., Simons L., Singh V., Smith V., Stinson J., Vagstad A.,
 Vanden R., Watanabe C., Wleand D., Woods K., Xie M.H., Yantusa D.,
 Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
 Godowski P.;
 RT "The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
 RT Effort to Identify Novel Human Secreted and Transmembrane Proteins: A
 RT Bioinformatics Assessment.";
 RL Genome Res. 13:2265-2270 (2003).
 DR EMBL: AY358914; AAQ89273.1; -.
 SQ SEQUENCE 243 AA; 26266 MW; BCB49AF4DBC03BC CRC64;

Query Match 100.0%; Score 243; DB 2; Length 243;
 Best Local Similarity 100.0%; Pred. No. 1.6e-220;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRPQGPASFORLRLGLLLLLLLQLPASSASELPKQKXALRORVNDLYNMCICQGA 60
 Db 1 MRPQGPASFORLRLGLLLLLLLQLPASSASELPKQKXALRORVNDLYNMCICQGA 60
 Qy 61 GVPGRGSPGANVTPTGPIPGRDGFKGKGEKCLRESFEESWTPNYKQCSMSLNYGIDL 120
 Db 61 GVPGRGSPGANVTPTGPIPGRDGFKGKGEKCLRESFEESWTPNYKQCSMSLNYGIDL 120
 Qy 121 GRIACETPTKMSNSALRYLFGSGLRLKCRNACCORWTFENGACSGPLIEATIIYDQ 180
 Db 121 GRIACETPTKMSNSALRYLFGSGLRLKCRNACCORWTFENGACSGPLIEATIIYDQ 180
 Qy 161 GSEPMNSTINIRHTSSVEGLCEGIGAGLVDAIWMGTCSDPKGDASTGMSVSRILIEE 240
 Db 161 GSEPMNSTINIRHTSSVEGLCEGIGAGLVDAIWMGTCSDPKGDASTGMSVSRILIEE 240
 Qy 241 LPK 243
 ||||
 Db 241 LPK 243

RESULT 3
 Q96CG8 PRELIMINARY; PRT; 243 AA.
 AC Q96CG8;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE Collagen triple helix repeat containing 1 (Collagen triple helix repeat-containing protein 1).

GN Name=CTHRC1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=2238257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Helel F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., Mesman P.J., McKernan K.J., Gale S., Garcia A.M., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz U., Myers R.W., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Watta M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Strausberg R.;
 RL Submitted (SSP-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Aorta smooth muscle;
 RA Lehnert W., Moore D.P., Harmon K.J., Mancini M.L., Lindner V.;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC014245; AAI14245.1; -.
 DR EMBL: AY136825; AAI15749.1; -.
 DR GeneW; HGNC:18831; CTRHCL.
 DR GO; GO:0005737; C:cytoplasm; IEA.
 DR GO; GO:0006817; P:phosphate transport; IEA.
 DR InterPro; IPR008161; C1g_helix.
 DR InterPro; IPR008160; Collagen.
 DR Pfam; PF01391; Collagen; 1.
 DR ProDom; PD000007; C1g_helix; 1.
 DR KX
 SQ SEQUENCE 243 AA; 26224 MW; A1FFEB1C66867F9 CRC64;

Query Match 70.0%; Score 170; DB 2; Length 243;
 Best Local Similarity 100.0%; Pred. No. 1.1e-151;
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 74 IPGTGPIPGRDGFKGKGEKCLRESFEESWTPNYKQCSMSLNYGIDLQSGTPTKMS 133
 Db 74 IPGTGPIPGRDGFKGKGEKCLRESFEESWTPNYKQCSMSLNYGIDLQSGTPTKMS 133
 Qy 134 NSALRYLFGSGLRLKCRNACCORWTFENGACSGPLIEATIIYDQSGSEPMNSTINIR 193
 Db 134 NSALRYLFGSGLRLKCRNACCORWTFENGACSGPLIEATIIYDQSGSEPMNSTINIR 193
 Qy 194 TSSVEGLCEGIGAGLVDAIWMGTCSDPKGDASTGMSVSRILIEELK 243
 Db 194 TSSVEGLCEGIGAGLVDAIWMGTCSDPKGDASTGMSVSRILIEELK 243

RESULT 4
 Q81X63 PRELIMINARY; PRT; 232 AA.
 ID Q81X63;
 AC Q81X63;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)

DT 01-MAR-2003 (TREMBlrel. 23, last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, last annotation update)
DE NTMCL
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Sanki N., Fujiki K., Kanai A., Tanaka Y., Iwata T.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF395488; AA017919.1; -
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0006817; P:phosphate transport; IEA.
DR InterPro; IPR008161; C1g helix.
DR InterPro; IPR008160; Collagen.
DR Pfam; PF01391; Collagen; 1.
DR ProDom; PD000007; C1g_helix; 1.
KW Collagen.
SQ SEQUENCE 232 AA; 25163 MW; E9D4BC30304837ED CRC64;

Query Match 69.5%; Score 169; DB 2; Length 232;
Best Local Similarity 100.0%; Pred. No. 9.4e-151;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 IGTGPIGRDGFKEGECLEESFESWTPTNYKQCSWSLWYGLDGLKIACTFTKMS 133
DB 60 IGTGPIGRDGFKEGECLEESFESWTPTNYKQCSWSLWYGLDGLKIACTFTKMS 119
QY 134 NSALRVLFSGSLRLKCRNACCORWYTFNGAECGSLPIEATIIYLDQSPENNSTINHR 193
DB 120 NSALRVLFSGSLRLKCRNACCORWYTFNGAECGSLPIEATIIYLDQSPENNSTINHR 179
QY 194 TSSVGEGLCGGIGAGLVDAVIAWGTGSDYRKGDASTWMSVSKIIIEELP 242
DB 180 TSSVGEGLCGGIGAGLVDAVIAWGTGSDYRKGDASTWMSVSKIIIEELP 228

RESULT 5

Q8CG08 PRELIMINARY; PRT; 245 AA.
ID Q8CG08;
AC Q8CG08;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, last annotation update)
DE Collagen triple helix repeat-containing protein 1.
DR Name=Ctrcl;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Sprague-Dawley; TISSUE=8 day balloon-injured carotid artery;
RA Lehnert W., Moore D.P., Harmon K.J., Mancini M.L., Lindner V.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY136824; AAM15748.1; -
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0006817; P:phosphate transport; IEA.
DR InterPro; IPR008161; C1g helix.
DR InterPro; IPR008160; Collagen.
DR Pfam; PF01391; Collagen; 1.
DR ProDom; PD000007; C1g_helix; 1.
KW Collagen.
SQ SEQUENCE 245 AA; 26424 MW; 2296FD6DCDBA21F2 CRC64;

Query Match 45.7%; Score 111; DB 2; Length 245;
Best Local Similarity 100.0%; Pred. No. 4.9e-96;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 IGTGPIGRDGFKEGECLEESFESWTPTNYKQCSWSLWYGLDGLKIACTFTKMS 133
DB 76 IGTGPIGRDGFKEGECLEESFESWTPTNYKQCSWSLWYGLDGLKIACTFTKMS 135

QY 134 NSALRVLFSGSLRLKCRNACCORWYTFNGAECGSLPIEATIIYLDQSP 184
DB 136 NSALRVLFSGSLRLKCRNACCORWYTFNGAECGSLPIEATIIYLDQSP 186

RESULT 6

Q9D1D6 PRELIMINARY; PRT; 245 AA.
ID Q9D1D6
AC Q9D1D6;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, last annotation update)
DE Mus musculus 18-day embryo whole body cDNA, RIKEN full-length enriched library, clone:1110014807 product:hypothetical Collagen triple helix repeat containing protein, full insert sequence.
DE repeat containing protein, full insert sequence.
GN Name=Ctrcl;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=whole body;
RC MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=whole body;
RC MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
RN [3]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=whole body;
RC The FANTOM Consortium;
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
RN [4]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=whole body;
RC MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630 (2000).
RN [5]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=whole body;
RC MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Kono H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kasaiwa K., Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771 (2000).
RN [6]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=whole body;
RC Akiyama T., Arai A., Aono H., Arahata T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M., Hangaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F., Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,

RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
 RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Nunazaki R., Ohno M.,
 RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
 RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
 RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
 RA Teijima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
 RA Muramatsu M., Hayashizaki Y.,
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK003674; BAB22930.1; -
 DR MGD; MGI:1915838; Cbhrcl.
 DR GO; GO:0005737; Cytochrome, IIA.
 DR GO; GO:0006817; P-phosphate transport; IEA.
 DR InterPro; IPR008161; C1g_helix.
 DR InterPro; IPR008160; Collagen.
 DR Pfam; PF01391; Collagen, 1.
 DR ProDom; PD000007; C1g_helix; 1.
 DR Collagen; Hypothetical protein.
 SQ SEQUENCE 245 AA; 26460 MW; 14951B87D8181A0E CRC64;

Query Match 45.7%; Score 111; DB 2; Length 245;
 Best Local Similarity 100.0%; Pred. No. 4.9e-96;
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 IPGTGPIGRDGFGEKGEKLESEFESEWTPNYQCWSLNYGIDIGKIAECTFTYMS 133
 |||||
 DB 76 IPGTGPIGRDGFGEKGEKLESEFESEWTPNYQCWSLNYGIDIGKIAECTFTYMS 135

QY 134 NSAIRVLFSSGLRLKRCNACCORWYFTFNGAECGSPLEIITYLDGSGPE 184
 |||||
 DB 136 NSAIRVLFSSGLRLKRCNACCORWYFTFNGAECGSPLEIITYLDGSGPE 186

RESULT 7
 O6H8C6 PRELIMINARY; PRT; 53 AA.
 AC O6H8C6; PRELIMINARY; PRT; 53 AA.
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DE 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Hypothetical protein OUI006_A02.39.
 GN Name-OUI006_A02.39.
 OS Oryza sativa (Japanese cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eriaristidae; Oryzaceae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sasaki T., Matsumoto T., Yamamoto K.,
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF003977; BAD25023.1; -
 DR Hypothetical protein.
 KW
 SQ SEQUENCE 53 AA; 5363 MW; 7A0775BFC5C7A683 CRC64;

Query Match 3.7%; Score 9; DB 2; Length 53;
 Best Local Similarity 100.0%; Pred. No. 2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 LLLLLLLOL 24
 |||||
 DB 22 LLLLLLLOL 30

RESULT 8
 O6IH72 PRELIMINARY; PRT; 86 AA.
 AC O6IH72;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE HPC03105.
 GN ORENames=HDC03105;
 OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA PubMed=14709175;
 RA Hild M., Beckmann B., Haas S., Solov'yev V., Busold C.,
 RA Fellenberg K., Boutros M., Vingron M., Sauer F., Hohenberg J., Piro R.,
 RT "An integrated gene annotation and transcriptional profiling approach
 towards the full gene content of the Drosophila genome.";
 RL Genome Biol. 5:R3-R3(2003).
 CC -1- MISCELLANEOUS: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ third party annotation (TPA) entry.
 DR EMBL; BK003544; DAA03743.1; -
 SQ SEQUENCE 86 AA; 9918 MW; E7E62A6DFAD94D40 CRC64;

Query Match 3.7%; Score 9; DB 2; Length 86;
 Best Local Similarity 100.0%; Pred. No. 3.1;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 LLLLLLLOL 24
 |||||
 DB 39 LLLLLLLOL 47

RESULT 9
 O6ILS3 PRELIMINARY; PRT; 86 AA.
 AC O6ILS3;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DE 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE HDC08497.
 GN ORENames=HDC08497;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA PubMed=14709175;
 RA Hild M., Beckmann B., Haas S., Solov'yev V., Busold C.,
 RA Fellenberg K., Boutros M., Vingron M., Sauer F., Hohenberg J., Piro R.,
 RT "An integrated gene annotation and transcriptional profiling approach
 towards the full gene content of the Drosophila genome.";
 RL Genome Biol. 5:R3-R3(2003).
 CC -1- MISCELLANEOUS: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ third party annotation (TPA) entry.
 DR EMBL; BK001943; DAA02788.1; -
 SQ SEQUENCE 86 AA; 9651 MW; DBE5E1028CA12B3 CRC64;

Query Match 3.7%; Score 9; DB 2; Length 86;
 Best Local Similarity 100.0%; Pred. No. 3.1;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 LLLLLLLOL 24
 |||||
 DB 45 LLLLLLLOL 53

RESULT 10
 O6IUT6 PRELIMINARY; PRT; 96 AA.
 AC O6IUT6;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE HDC14245.
 GN ORENames=HDC14245;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

```

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14709175;
RA Hild M., Beckmann B., Haas S., Koch B., Solovjev V., Busold C.,
RA Fellenberg K., Boulton M., Vingron M., Sauer F., Hobeisel J., Paro R.;
RT "An integrated gene annotation and transcriptional profiling approach
RT towards the full gene content of the Drosophila genome.";
RL Genome Biol. 5:R3-R3(2003).
CC -1- MISCELLANEOUS: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ third party annotation (TPA) entry.
DR EMBL; BK002630; DAA04136.1; -
SQ SEQUENCE 96 AA; 11039 MW; BFCBICDCC3F1B6DD CRC64;

Query Match 3.7%; Score 9; DB 2; Length 96;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 16 LLLLLLLOL 24
Db 7 LLLLLLLOL 15

RESULT 11
O61G45 PRELIMINARY; PRT; 105 AA.
ID O61G45
AC O61G45;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE HDCC07244;
GN ORFNames=HDC07244;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14709175;
RA Hild M., Beckmann B., Haas S., Koch B., Solovjev V., Busold C.,
RA Fellenberg K., Boulton M., Vingron M., Sauer F., Hobeisel J., Paro R.;
RT "An integrated gene annotation and transcriptional profiling approach
RT towards the full gene content of the Drosophila genome.";
RL Genome Biol. 5:R3-R3(2003).
CC -1- MISCELLANEOUS: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ third party annotation (TPA) entry.
DR EMBL; BK003921; DAA02619.1; -
SQ SEQUENCE 105 AA; 11424 MW; F655A4D40747519D CRC64;

Query Match 3.7%; Score 9; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 16 LLLLLLLOL 24
Db 14 LLLLLLLOL 22

RESULT 12
CON2_HUMAN STANDARD; PRT; 120 AA.
ID CON2_HUMAN
AC O43555; Q9BYN9; Q9BYP0;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Progonaoliberin II precursor (contains: Gonadoliberin II (LH-RH II)
DE [luteinizing hormone-releasing hormone II] (Gonadotropin-releasing
DE hormone II) (LH-RH II) (LH-RH II); GnRH-associated peptide II).
GN Name=GNRH2;
OS Homo sapiens (Human).

```

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=98081869; PubMed=9419371;
RA White R.B., Eisen J.A., Kaestli T.L., Fernald R.D.;
RT "Second gene for gonadotropin-releasing hormone in humans.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:305-309(1998).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1, 2 AND 3).
RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baggaley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Bead L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grahame D.V., Griffiths C., Griffiths M.N.D., Gilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Lehaeashah M.H., Leverha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConachie I.J., McElroy K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Pratchlingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.B., Sehra H.K., Showkhen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M., Williams S.A.,
RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Bentley D.R., Beck S.,
RA Wilting L., Way P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
CC -1- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates
CC the secretion of both luteinizing and follicle-stimulating
CC hormones.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=alternative splicing; Named isoforms=3;
CC Comment=Experimental confirmation may be lacking for some
CC isoforms;
CC Name=1;
CC IsoId=O43555-1; Sequence=Displayed;
CC Name=2;
CC IsoId=O43555-2; Sequence=VSP_001825;
CC Name=3;
CC IsoId=O43555-3; Sequence=VSP_001826;
CC -1- TISSUE SPECIFICITY: Midbrain; expressed at significantly higher
CC levels outside the brain (up to 30-fold), particularly in the
CC kidney, bone marrow and prostate.
CC -1- SIMILARITY: Belongs to the GnRH family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
DR EMBL; AF036329; AAC02980.1; -
DR EMBL; AF036330; AAC02981.1; -
DR EMBL; AL121905; CAC10338.1; -
DR EMBL; AL121905; CAC29100.1; -
DR EMBL; AL121905; CAC29101.1; -
DR GeneW; HGNC:4420; GNRH2.
DR MIM; 602352; -

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DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Hypothetical protein C02F4.3.
GN Name=C02F4.3;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCB1_taxid=6239;
RN
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RL investigating biology."
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Cummings P.N.;
RL Submitted (Oct-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z81032; CAB02722.1; -.
DR PIR; T18867; T18867.
DR WormPep; C02F4.3; CE07854.
KW Hypothetical protein.
SQ SEQUENCE 144 AA; 16112 MW; 907F9DDBIACC1762 CRC64;
OY 16 LLLLLLQL 24
   |||||
   |||||
Db 67 LLLLLLQL 75

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Search completed: December 25, 2004, 05:32:53
 Job time : 97 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 25, 2004, 05:31:17 ; Search time 497 Seconds
(without alignments)
2566.618 Million cell updates/sec

Title: US-10-063-734-122

Perfect score: 1301
Sequence: 1 MRPQPASPORTRLGILL.....GDASTGMSVSRITIEELPK 243

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4134886 segs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Command line parameters:

-MODEL=frame+g2n.model -DEV=x1h
-O=/cgn2.1/USPTO.epool/US10063734/runat_22122004_101733_8913/app_query.fasta_1.391
-DB=N Geneseq_23Sep04 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPEXT=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi
-LIST=100 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=50
-NODE=LOCAL -OUTFMT=ptc -NORF=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10063734 @CEN_1_1470 @runat_22122004_101733_8913 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEOQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

N_Geneseq_23Sep04:*
1: geneseqn1908:*
2: geneseqn1908:*
3: geneseqn2000as:*
4: geneseqn2000as:*
5: geneseqn2000as:*
6: geneseqn2000as:*
7: geneseqn2000as:*
8: geneseqn2000as:*
9: geneseqn2000as:*
10: geneseqn2000as:*
11: geneseqn2000as:*
12: geneseqn2000as:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1301	100.0	729	6	ABSG4029
2	1301	100.0	729	10	ABT33241
3	1301	100.0	729	11	ADU93173
4	1301	100.0	732	6	ABV99144
5	1301	100.0	732	6	ABSG4028
6	1301	100.0	732	10	ABT33240

7	1301	100.0	732	11	ADL93172
8	1301	100.0	837	6	ABV99145
9	1301	100.0	837	6	ABSG4030
10	1301	100.0	837	6	ABSG4031
11	1301	100.0	837	10	ABT33242
12	1301	100.0	837	10	ABT33243
13	1301	100.0	837	11	ADL93174
14	1301	100.0	837	11	ADL93175
15	1301	100.0	1256	10	ADB90997
16	1301	100.0	1257	3	AA337144
17	1301	100.0	1257	4	AA54507
18	1301	100.0	1257	4	AA546107
19	1301	100.0	1257	4	AA546107
20	1301	100.0	1257	6	AB574438
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30	1301	100.0	1257	6	AB574438
31	1301	100.0	1257	6	AB574438
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33	1301	100.0	1257	6	AB574438
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35	1301	100.0	1257	6	AB574438
36	1301	100.0	1257	6	AB574438
37	1301	100.0	1257	6	AB574438
38	1301	100.0	1257	6	AB574438
39	1301	100.0	1257	6	AB574438
40	1301	100.0	1257	6	AB574438
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74	1301	100.0	1257	6	AB574438
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76	1301	100.0	1257	6	AB574438
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80 1301 100.0 1257 8 ACC86274 Acc86274 Human sec
81 1301 100.0 1257 8 ACC45209 Acc45209 Human sec
82 1301 100.0 1257 8 ACC90146 Acc90146 Human sec
83 1301 100.0 1257 8 ACC12754 Acc12754 Human sec
84 1301 100.0 1257 8 ACC19984 Acc19984 Human sec
85 1301 100.0 1257 8 ABX76928 ABX76928 Human PRO
86 1301 100.0 1257 8 ACA73260 ACA73260 Human hum
87 1301 100.0 1257 8 ACA68803 ACA68803 Novel hum
88 1301 100.0 1257 8 ACA74647 ACA74647 CDNA enco
89 1301 100.0 1257 8 ACA70514 ACA70514 Human sec
90 1301 100.0 1257 8 ACC14700 ACC14700 Human PRO
91 1301 100.0 1257 8 ACA83757 ACA83757 Human CDN
92 1301 100.0 1257 8 ACA83757 ACA83757 Human CDN
93 1301 100.0 1257 8 ABX98837 ABX98837 Novel hum
94 1301 100.0 1257 8 ACA67331 ACA67331 CDNA enco
95 1301 100.0 1257 8 ACC81314 ACC81314 Human sec
96 1301 100.0 1257 8 ACA95638 ACA95638 Novel hum
97 1301 100.0 1257 8 ACC04556 ACC04556 Novel hum
98 1301 100.0 1257 8 ACC87997 ACC87997 Human sec
99 1301 100.0 1257 8 ACC12659 ACC12659 Human sec
100 1301 100.0 1257 8 ACH66304 ACH66304 Novel hum
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ALIGNMENTS

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RESULT 1
ABSE4029
ID ABSE4029 standard; cDNA; 729 BP.
XX
XX ABSE4029;
AC
XX 15-NOV-2002 (first entry)
DT
XX Human breast tumour polynucleotide #478.
DE
XX Human; breast tumour protein; gene; ss; breast cancer; cytostatic;
KW vaccine.
XX
XX Homo sapiens.
OS
XX US2002085998-A1.
FN
XX
XX 04-JUL-2002.
PD
XX 13-APR-2001; 2001US-00834759.
PE
XX
XX 28-DEC-1998; 98US-00222575.
PR 02-APR-1999; 99US-00285480.
PR 23-JUN-1999; 99US-00339338.
PR 02-SEP-1999; 99US-00389681.
PR 03-NOV-1999; 99US-00433826.
PR 17-APR-2000; 2000US-0051621.
PR 08-JUN-2000; 2000US-00590751.
PR 22-JUL-2000; 2000US-00604287.
PR 20-JUL-2000; 2000US-00620405.
XX
XX (CORI-) CORIXA CORP.
PA
XX Jiang Y, Dillon DC, Mitcham JL, Xu J, Harlocker SL, Hepler WT;
PI Henderson RA;
XX WPI; 2002-635657/68.
DR P-PSDB; ABG78938.
XX
XX Novel breast cancer polynucleotides and polypeptides encoded by the
PT polynucleotides, useful for detecting the presence of breast cancer in a
PT patient, and in pharmaceutical compositions, for treating breast cancer.
XX Claim 1; Page 234; 247pp; English.
XX
XX The invention relates to an isolated breast tumour polynucleotide and the
CC polypeptide it encodes. The polynucleotide and polypeptide are useful for
CC detecting the presence of breast cancer in a patient, and in
```

CC pharmaceutical compositions for treating breast cancer. The sequences are
CC useful for stimulating an immune response in a patient and can therefore
CC be used in production of vaccines. The sequences are also useful for
CC detecting the presence of a cancer in a patient, by obtaining a
CC biological sample from the patient, contacting the biological sample with
CC a composition of the invention and detecting the amount of polynucleotide
CC that hybridizes to the sample. This sequence represents a human breast
CC tumour polynucleotide of the invention

XX Sequence 729 BP; 182 A; 162 C; 204 G; 181 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1,296-104 Length: 729
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conserved: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-10-063-734-122 (1-243) x ABSE4029 (1-729)

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QY 1 MetATGProGInGlyProAlaAlaSerProGInaArgLeuArgGlyLeuLeuLeu 20
Db 1 ATGCGACCCCGAGGCGCCCGCCCTCCCGAGCGGCTCCGCGGCTCGTGTCTCTG 60
QY 21 LeuLeuGInLeuProAlaProSerSerAlaSerGluLeuProGlyGlyGlyGlyAla 40
Db 61 CTGCTGCGAGCTCCCGCGCCCTCCAGCGCCTCTGAGATCCCGAAGGGAAGCAAGGGG 120
QY 41 GInLeuArgGInaArgGluValAlaAspLeuTyrAsnGlyMetCysLeuGInGlyProAla 60
Db 121 CAGCTCCGCGCAGAGGAGGTGTGCTGCTGATATATAGAAATGTGCTTACAGGCGCAGA 180
QY 61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
Db 181 GGAGTGGCTGTGTCAAGACGGAGCGCTGGGGCCAAATGTATTCGGGTCACCTGGGATC 240
QY 81 ProGlyArgAspGlyPheGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100
Db 241 CCAAGTGGGAGTGTATTCAGAGGAAAGGAGGAAATGTCTGAGGAAAGCTTTGAGGAG 300
QY 101 SerThrProAsnTyrGlyGlnCysSerTyrSerSerLeuAsnTyrGlyIleAspLeu 120
Db 301 TCCGTGACACCCCACTCAAGCAGTGTTCATGAGTTCAATGATATATATGACATGATCTT 360
QY 121 GlyLysIleAlaGluCysThrPheThrIleMetArgSerAsnSerAlaLeuArgValLeu 140
Db 361 GGGAAATTTGGGAGGTGTACATTACAAAGATGCTTCAAAATAGTCTCTAAGAGTTTG 420
QY 141 PheSerGlySerLeuArgLeuGlyCysArgAsnAlaCysCysGlnArgTyrPheThr 160
Db 421 TTCAGTGGCTCACTGGCTGCTAAATGCAAAATGCTGTCAGGTTGCTGATTTTACCA 480
QY 161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleTyrLeuAspGln 180
Db 481 TTCATGAGACTAAATGTTCCAGACCTCTCCCATTTGAAGCTATATATTATTTGACCA 540
QY 181 GlySerProGluLeuIleAsnSerThrIleAsnIleHisArgThrSerSerValGluLeu 200
Db 541 GGAAGCCTGAAATGAAATTCATTAACATTAATTCATGACCTTCTCTGTGGAAGACTT 600
QY 201 CysGInGlyIleGlyAlaGlyLeuValAspValAlaIleTyrValGlyThrCysSerAsp 220
Db 601 TGTGAAGAAATGTGTGTGATTAAGAGATGTTGATTTGGATTTGGCACTTTGATCAAT 660
QY 221 TyrProGlyIleAspAlaSerThrGlyTyrPheSerValSerArgIleIleGluGlu 240
Db 661 TACCAAAAGAAAGATGCTTCTACTGATGAATTCAGTTTCGCGATCATTTATGAGAA 720
QY 241 LeuProLys 243
Db 721 CTACCAAAA 729
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RESULT 2
ABT33241
ID ABT33241 standard; DNA; 729 BP.
XX
XX ABT33241;
AC
XX
XX 15-MAY-2003 (first entry)
DT
XX Human tumour-related DNA sequence - SEQ ID NO 511.
DE
XX
XX Human; ds; vaccine; gene therapy; T cell stimulation; T cell expansion;
KM tumour; breast cancer; cancer; immune response stimulation.
XX
XX Homo sapiens.
OS
XX WO200283956-A1.
XX
XX 24-OCT-2002.
XX
XX 15-APR-2002; 2002MO-US012378.
XX
XX 13-APR-2001; 2001US-00834759.
XX 07-DEC-2001; 2001US-00007805.
XX 13-FEB-2002; 2002US-00076622.
XX
XX (CORI-) CORIXA CORP.
XX
XX Houghton RL, Sleath PR, Persing DH, Jiang Y, Dillon DC,
PI Mitcham JL, Xu J, Harlocker SL, Hepler WT, Henderson RA, Fanger GR,
PI Vedvick TS, McNeill PD, Durham M;
XX
XX WPI; 2003-103376/09.
XX
XX New polypeptide and polynucleotide useful for stimulating and/or
PT expanding T cells specific for a tumor protein and treating breast
XX cancer.
XX
XX Example 1; Page 320; 375pp; English.
XX
XX The invention comprises a method of stimulating and/or expanding T cells
CC specific for a tumour protein. The invention further comprises human
CC nucleic acids and proteins that are associated with tumours (e.g. breast
CC cancer). The method and sequences of the invention are useful for
CC stimulating and/or expanding T cells specific for a tumour protein,
CC detecting the presence of cancer, stimulating an immune response in a
CC patient and treating breast cancer. The present DNA sequence represents a
CC human tumour-related DNA sequence
XX
XX
SQ Sequence 729 BP; 182 A; 162 C; 204 G; 181 T; 0 U; 0 Other;
XX
XX
Alignment Scores:
Pred. No.: 1.29e-104 Length: 729
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0
XX
US-10-063-734-122 (1-243) x ABT33241 (1-729)
QY 1 MetATGProGlnGlyProAlaIaSerProGlnATGLeuATGLeuLeuLeuLeu 20
DB 1 ATGCGACCCCGAGGCCCCCGCTCCCGCGACGGGCTCCGCGCTCTGCTCTG 60
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluLeuProLysGlyGlnLysAla 40
DB 61 CTGCTGCACTGCGCGCGCGCTCGACGCTCTGACATCCCCAAGGGAAGCAAGGCG 120
QY 41 GlnLeuATGlnATGATGlnValValaAlaPheLysTyrAerGlyMetCysLeuGlnGlyProAla 60
DB 121 CAGCTCCGCGAGAGGAGGTGGTGGACCTGTATTAAGATGTCTTACAGGCGCAGCA 180
QY 61 GlyValProGlyATGATGATGATGATGATGATGATGATGATGATGATGATGAT 80
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DB 181 GGAGTGCCTGATCGAGAGGAGGCCCTGGGGCAATGTTATTCGGGGTACACTGGGATC 240
QY 81 ProGlyATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 100
DB 241 CCAGCTCCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
QY 101 SerTPTTProATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
DB 301 TCTTGACACCCCACTACAGCAGTGTTCATGAGATTCATGATGATGATGATGATGAT 360
QY 121 GlyValIleAlaGluCysThrPheThrIleAsnIleHisArgThrSerValGluLys 140
DB 361 GGGAAATTTGCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
QY 141 PheSerGlySerLeuATGATGATGATGATGATGATGATGATGATGATGATGATGAT 160
DB 421 TTCAGTGGCTCATTCTGCTTAAATGCAAGATGATGATGATGATGATGATGATGAT 480
QY 161 PheATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
DB 481 TTCATATGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
QY 181 GlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerValGluLys 200
DB 541 GGAACCCCTGAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
QY 201 CysGlnGlyIleGlyAlaGlyLeuValAlaIleTyrValGlyThrCysSer 220
DB 601 TGTGAAGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
QY 221 TyrProLysGlyATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
DB 661 TACCAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
QY 241 LeuProLys 243
DB 721 CTACCAAAA 729
XX
XX
RESULT 3
ADL93173
ID ADL93173 standard; cDNA; 729 BP.
XX
XX ADL93173;
AC
XX 20-MAY-2004 (first entry)
DT
XX
XX Human breast cancer-associated polypeptide cDNA #475.
DE
XX
XX gene therapy; protein therapy; vaccine; breast cancer; cancer; human; ss;
KM gene.
XX
XX Homo sapiens.
OS
XX US2003166022-A1.
XX
XX 04-SEP-2003.
XX
XX 15-APR-2002; 2002US-00124805.
XX
XX 28-DEC-1998; 98US-00222575.
XX 02-APR-1998; 98US-00285480.
XX 23-JUN-1999; 99US-00393380.
XX 02-SEP-1999; 99US-00389681.
XX 03-NOV-1999; 99US-00433826.
XX 17-APR-2000; 2000US-00551621.
XX 08-JUN-2000; 2000US-00590751.
XX 22-JUN-2000; 2000US-00604287.
XX 20-JUL-2000; 2000US-00620405.
XX 13-APR-2001; 2001US-00834759.
XX 07-DEC-2001; 2001US-00007805.
XX 13-FEB-2002; 2002US-00076622.
XX
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PA (CORI-) CORIXA CORP.
XX
XX Houghton RL, Sleath PR, Persing DH,
XX
XX WPI: 2003-874918/81.
XX
XX An isolated oncogenic polypeptide useful for preventing, diagnosing and
XX treating breast cancer.
XX
XX Example 1; SEQ ID NO 511; 294bp; English.
XX
XX The invention relates to an isolated breast cancer-associated
XX polypeptide. The polypeptide may be used for the diagnosis and treatment
XX of breast cancers. The methods are useful for detecting the presence of a
XX cancer in a patient and treating a cancer in a patient. The present
XX sequence represents cDNA encoding a human breast cancer-associated
XX polypeptide.
XX
XX Sequence 729 BP; 182 A; 162 C; 204 G; 181 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 1.29e-104 Length: 729
XX Score: 1301.00 Matches: 243
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 100.00% Indels: 0
XX DB: 11 Gaps: 0
XX
XX US-10-063-734-122 (1-243) x ADL93173 (1-729)
XX
XX 1 MetArgProGlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeu 20
XX 1 ATGCGACCCAGGAGCCCGCCGCTCCCGACAGGCTCGCGCCCTCTGCTGCTCG 60
XX
XX 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGlnIleProGlyGlyGlnGlnAla 40
XX 61 CTGCTGACAGCTGCGCGCGCTGAGACGCTCTGAGATCCCAAGGAGGAGGAGGCG 120
XX
XX 41 GlnLeuArgGlnArgGlnValValAlaPLeuTyraGlnIleMetCysLeuGlnGlyProAla 60
XX 121 CAGCTCCGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
XX
XX 61 GlyValProGlyArgGlnGlySerProGlyValAlaSerValIleProGlyThrProGlyIle 80
XX 181 GAGAGTCCCTGCTGAGACGCGGAGCCCTGGGAGCCAAATGTAATTCGAGTACACCTGAGATC 240
XX
XX 81 ProGlyArgGlnGlyPheLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100
XX 241 CCAAGTCCGAGATGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
XX
XX 101 SerTyrThrProAsnTyrIleGlnCysSerTyrPheSerLeuAsnTyrGlyIleAspLeu 120
XX 301 TCTCGACACCCACCACTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
XX
XX 121 GlyIleIleAlaGluCysThrPheThrIleSMeTArgSerAsnSerAlaLeuArgValLeu 140
XX 361 GGGAAATTTGGGAGAGTGTACATTTCAGAAAGAGCTTCAATAGTCTCTAAGAGTTTG 420
XX
XX 141 PheSerGlySerLeuArgLeuLeuGlyCysArgGlnAlaCysGlyGlnArgTyrPheThr 160
XX 421 TTCAGTGGCTCACTTGGCTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
XX
XX 161 PheAsnGlyIleAlaGluCysSerGlyProLeuProIleGlnAlaIleIleTyrLeuAspGln 180
XX 481 TTCAATGAGAGTGAATGTTCAAGACCTTCCCATTTGAAGCTAATTAATTTATTTGACCAA 540
XX
XX 181 GlySerProGlnMetLeuSerThrIleAsnIleHisArgThrSerSerValGlnGlyLeu 200
XX 541 GGAAGCCCTGAAAGAAATTCACATTAATTCATGCACTTCTTCTGAGAGAGAGCTT 600
XX
XX 201 CysGlnGlyIleGlyValAlaGlyLeuValAspValAlaIleTyrValGlyThrCysSerAsp 220
XX 601 TGTGAAGAAATTTGTTGCTGATGATGAGATGATGATGATGATGATGATGATGATGATGAT 660

QY 221 TyrProGlyGlyAspAlaSerThrGlyTyrPheAsnValSerArgIleIleIleGlnGlu 240
DB 661 TACCCAAAG 720
QY 241 LeuProGly 243
DB 721 CTACCAAAA 729
RESULT 4
ID ABV99144 standard; cDNA, 732 BP.
AC ABV99144;
XX 14-JAN-2003 (first entry)
XX
XX Human pancreatic cancer expressed cDNA SEQ ID NO 4556.
XX
XX Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;
XX cytostatic; tumour; gene; ss.
XX Homo sapiens.
XX WO200260317-A2.
XX
XX 08-AUG-2002.
XX
XX 30-JAN-2002; 2002WO-US002781.
XX
XX 30-JAN-2001; 2001US-0265305P.
XX 31-JAN-2001; 2001US-0265682P.
XX 09-FEB-2001; 2001US-0267868P.
XX 21-MAR-2001; 2001US-0278651P.
XX 28-APR-2001; 2001US-0287112P.
XX 16-MAY-2001; 2001US-0291631P.
XX 12-JUL-2001; 2001US-0305484P.
XX 20-AUG-2001; 2001US-0313999P.
XX 27-NOV-2001; 2001US-0333626P.
XX
XX (CORI-) CORIXA CORP.
XX
XX Benson DR, Kalos MD, Lodes MJ, Persing DH, Hepler WT, Jiang Y,
XX WPI: 2002-627435/67.
XX P-PSDB; ABP66636.
XX
XX New isolated polynucleotide and pancreatic tumor polypeptides, useful for
XX diagnosis, preventing and/or treating cancer, particularly pancreatic
XX cancer.
XX
XX Example 11; SEQ ID NO 4556; 300bp + Sequence Listing; English.
XX
XX The invention relates to an isolated polynucleotide (1) comprising: (a)
XX any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b)
XX residues of (a); (c) sequences consisting of at least 20 contiguous
XX stringent conditions; (d) sequences that hybridize to (a) under moderately
XX to (a); or (e) degenerate variants of (a). Polypeptides (ABP668596-
XX ABP66637) encoded by (1) and oligonucleotide can be used to detect cancer
XX in a patient and compositions comprising polypeptides, polynucleotides,
XX antibodies, fusion proteins, T cell populations and antigen presenting
XX cells expressing the polypeptide are useful in treating pancreatic cancer
XX and stimulating an immune response. The polynucleotides can be used as
XX probes or primers for nucleic acid hybridization. In the design and
XX preparation of ribozyme molecules for inhibiting expression of the tumour
XX polypeptides and proteins in the tumour cells, in vaccines and for gene
XX therapy. Note: The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 732 BP; 184 A; 162 C; 204 G; 182 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1,29e-104 Length: 732
 Score: 1301.00 Matches: 243
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 Gaps: 0

US-10-063-734-122 (1-243) x ABV99144 (1-732)

QY 1 MetAArgProGInGlyProAlaAlaSerProGInAArgLeuArgGlyLeuLeuLeuLeu 20
 DB 1 ATGCCGACCCAGGGCCCCCGCCCTCCCGCAGCGGCTCCGCGCTCTGCTGCTCTG 60
 QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGlnLeuProGlyGlyGlyGlyGly 40
 DB 61 CTGCTGACACTGCGCCGCGCTGAGCGCTTGAAGATCCCAAGGAGCAAAAGGGGG 120
 QY 41 GlnLeuArgGlnArgGlnValValAspLeuTyrAsnGlyMetCysLeuGlnGlyProAla 60
 DB 121 CAGCTCCGCGAGAGAGGTGTGTGACCTGTATTAATGATGTGCTTACAGGCGCAGCA 180
 QY 61 GlnValProGlyAArgAspGlySerProGlyAlaAsnValLeuProGlyTyrProGly 80
 DB 181 GGAGTCTCTGTGACAGCGGAGCCCTGGGGCCAAATGTTATTCGGGTACACTGGGATC 240
 QY 81 ProGlyAArgAspGlyPheGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100
 DB 241 CCAAGTCGGAGATGATTCAGAAAGAGAAAGGGGAAATGCTGAGGAAAGCTTGGAGAG 300
 QY 101 SerTrpThrProAsnTyrIleGlnCysSerTrpSerSerLeuAsnTyrGlyIleAspLeu 120
 DB 301 TCTGTGACACCCACACTACAGACAGTGTTCATGAGTTCATTGAATTAATGCAATGATCTT 360
 QY 121 GlnValGlnAlaGlnCysTrpPheTrpIleMetArgSerAsnSerAlaLeuArgValLeu 140
 DB 361 GGGAAATATGGAGAGTGTACATTACAAAGATCGTTCAAAATGTCCTTAAAGATTTTG 420
 QY 141 PheSerGlySerLeuArgLeuLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 160
 DB 421 TTCAGTGGCTCACTTGGCTTAAATGCAAGAAAGCATGCTGACGGTGTGATTTTCACA 480
 QY 161 PheAsnGlyAlaGlnCysSerGlyProLeuProGlnAlaIleIleTyrIleAspGln 180
 DB 481 TTCAATGAGAGCTCAATGTTCAAGACCTCTCCATTGAACTTAATTTTGGACCA 540
 QY 181 GlnSerProGlnMetAsnSerThrIleAsnIleIleArgThrSerSerValGlnGlyLeu 200
 DB 541 GGAAGCCCTGAATGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 600
 QY 201 CysGlnGlyIleGlyAlaGlyLeuValAspValAlaIleTrpValGlyThrCysSerAsp 220
 DB 601 TGTGAAGGAATGCTGCTGATTAAGTGAATGTTGCTGATGCTGCTGCTGCTGCTGCTG 660
 QY 221 TyrProGlyGlyAspAlaSerThrGlyTrpAsnSerValSerArgIleIleIleGlnGln 240
 DB 661 TACCCTCAAAAGAGATGCTTCTACTGAGATGGAATTCAGTTTCTGCATCATTTATTAAGA 720
 QY 241 LeuProGly 243
 DB 721 CTACCAAAA 729

RESULT 5
 ABS64028
 ID ABS64028 standard; cDNA; 732 BP.
 XX
 XX ABS64028;
 XX
 XX 15-NOV-2002 (first entry)
 XX
 XX Human breast tumour polynucleotide #477.
 XX
 XX Human breast tumour protein; gene; ss; breast cancer; cytostatic;
 KM Human; breast tumour protein; gene; ss; breast cancer; cytostatic;

vaccine.

XX Homo sapiens.

XX US2002085998-A1.

XX 04-JUL-2002.

XX 13-APR-2001; 2001US-00834759.

XX 28-DEC-1998; 98US-00222575.

XX 02-APR-1999; 99US-00285480.

XX 23-JUN-1999; 99US-00339338.

XX 02-SEP-1999; 99US-00389681.

XX 03-NOV-1999; 99US-00433826.

XX 17-APR-2000; 2000US-00551621.

XX 08-JUN-2000; 2000US-00590751.

XX 22-JUN-2000; 2000US-00604287.

XX 20-JUL-2000; 2000US-00620405.

XX (CORI-) CORIXA CORP.

XX Jiang Y, Dillon DC, Matcham JL, Xu J, Harlocker SL, Hepler WT;
 PI Henderson RA;
 PI
 DR WPI: 2002-635657/68.
 DR P-PSDB; ABG78938.

XX Novel breast cancer polynucleotides and polypeptides encoded by the
 PT polynucleotides, useful for detecting the presence of breast cancer in a
 PT patient, and in pharmaceutical compositions, for treating breast cancer.
 PS Claim 1; Page 234; 247pp; English.

XX The invention relates to an isolated breast tumour polynucleotide and the
 CC polypeptide it encodes. The polynucleotide and polypeptide are useful for
 CC detecting the presence of breast cancer in a patient, and in
 CC pharmaceutical compositions for treating breast cancer. The sequences are
 CC useful for stimulating an immune response in a patient and can therefore
 CC be used in production of vaccines. The sequences are also useful for
 CC detecting the presence of a cancer in a patient, by obtaining a
 CC biological sample from the patient, contacting the biological sample with
 CC a composition of the invention and detecting the amount of polynucleotide
 CC that hybridizes to the sample. This sequence represents a human breast
 CC tumour polynucleotide of the invention

XX Sequence 732 BP; 184 A; 162 C; 204 G; 182 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 1,29e-104 Length: 732
 Score: 1301.00 Matches: 243
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 Gaps: 0

US-10-063-734-122 (1-243) x ABS64028 (1-732)

QY 1 MetAArgProGInGlyProAlaAlaSerProGInAArgLeuArgGlyLeuLeuLeuLeu 20
 DB 1 ATGCCGACCCAGGGCCCCCGCCCTCCCGCAGCGGCTCCGCGCTCTGCTGCTCTG 60
 QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGlnLeuProGlyGlyGlyGlyGly 40
 DB 61 CTGCTGACACTGCGCCGCGCTGAGCGCTTGAAGATCCCAAGGAGCAAAAGGGGG 120
 QY 41 GlnLeuArgGlnArgGlnValValAspLeuTyrAsnGlyMetCysLeuGlnGlyProAla 60
 DB 121 CAGCTCCGCGAGAGAGGTGTGTGACCTGTATTAATGATGTGCTTACAGGCGCAGCA 180
 QY 61 GlnValProGlyAArgAspGlySerProGlyAlaAsnValLeuProGlyTyrProGly 80
 DB 181 GGAGTCTCTGTGACAGCGGAGCCCTGGGGCCAAATGTTATTCGGGTACACTGGGATC 240

Db 721 CTACCAAAA 729

|||||

RESULT 7
ADL93172
ID ADL93172 standard; cDNA; 732 BP.

XX
AC ADL93172;
XX
DT 20-MAY-2004 (first entry)

XX
DE Human breast cancer-associated polypeptide cDNA #474.
XX
KM gene therapy; protein therapy; vaccine; breast cancer; cancer; human; ss;
XX
OS Homo sapiens.
XX
PN US2003166022-A1.
XX
PD 04-SEP-2003.
XX
PF 15-APR-2002; 2002US-00124805.
XX
PR 28-DEC-1998; 98US-00222575.
XX
PR 02-APR-1999; 99US-00285480.
XX
PR 23-JUN-1999; 99US-00339338.
XX
PR 02-SEP-1999; 99US-00389681.
XX
PR 03-NOV-1999; 99US-00433826.
XX
PR 17-APR-2000; 2000US-00551621.
XX
PR 08-JUN-2000; 2000US-00590751.
XX
PR 22-JUN-2000; 2000US-00604287.
XX
PR 20-JUL-2000; 2000US-00629405.
XX
PR 13-APR-2001; 2001US-00834759.
XX
PR 07-DEC-2001; 2001US-00007805.
XX
PR 13-FEB-2002; 2002US-00076622.
XX
PA (CORI-) CORIXA CORP.
XX
PI Houghton RL, Sleath PR, Persing DH;
XX
DR WPI; 2003-874918/81.
XX
DR P-PSDB; ADL93176.
XX
XX
PT An isolated oncogenic polypeptide useful for preventing, diagnosing and
XX
PT treating breast cancer.
XX
XX
PS Example 1; SEQ ID NO 510; 294pp; English.
XX
XX
CC The invention relates to an isolated breast cancer-associated
XX
CC polypeptide. The polypeptide may be used for the diagnosis and treatment
XX
CC of breast cancers. The methods are useful for detecting the presence of a
XX
CC cancer in a patient and treating a cancer in a patient. The present
XX
CC sequence represents cDNA encoding a human breast cancer-associated
XX
CC polypeptide.
XX
SQ Sequence 732 BP; 184 A; 162 C; 204 G; 182 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.29e-104 Length: 732
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 11 Gaps: 0

US-10-063-734-122 (1-243) x ADL93172 (1-732)

QY 1 MetArgProGlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeuLeu 20
DB 1 ATGGCGACCCCGAGGCGCCCGGCTCCCGCAGCGGCTCCGCGCTCTGCTGCTCTG 60
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGlnLeuProGlyGlyGlnLeu 40

Db 61 CTGCTGACAGCTGCCCGCCCGCTCGAGCGCTCTGAGATCCCAAGGAGAAAAGGCG 120

QY 41 GlnLeuArgGlnArgGlnValValAspLeuTyrAsnGlyMetCysLeuGlnGlyProAla 60
DB 121 CAGCTCCGCGCAGAGGAGGTGTGAGCTGTATTAATGTGAAATGTGCTTACAAAGGCGCAGA 180

QY 61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyTyrProGlyIle 80
DB 181 GGAGTGCCTGCTCGAGACGGAGCCCTGGGCGCAATGTTATTCGGGTCACCTGGGATC 240

QY 81 ProGlyArgAspGlyPheLeuGlyGlyLeuGlyGlyGlyGlyGlyGlyGlyGlyGly 100
DB 241 CCAGTCCGCGAGATGATTTCAAGAGAAAAGGGGAAATGCTGAGGAAAGCTTTAGGAG 300

QY 101 SerTyrProAsnTyrIleGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 120
DB 301 TCCTGGACACCCCACTACAGCAGAGCTTCATGAGTTCATTAATTAATGCGATGATCTT 360

QY 121 GlyValIleAlaGluCysThrPheThrIleSerMetArgSerAsnSerAlaLeuArgValLeu 140
DB 361 GGAGAAATTCGCGAGTGTACATTTACAAAGATCGCTTCAAAATAGTGTCTTAAGAGTTTG 420

QY 141 PheSerGlySerLeuArgLeuLysCysArgAsnAlaCysCysGlnArgTyrPheThr 160
DB 421 TTCAGTGGCTCACTTCGGCTAAATGCAAAATGATGATGCTGACAGCTTGATTTTACA 480

QY 161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleTyrLeuAspGln 180
DB 481 TTCAAATGAGCTGAATGTTCAGAGACCTCTCCCATTTGAAGCTATTAATTTTGAACCA 540

QY 181 GlySerProGlnMetAsnSerThrIleAsnIleHisArgThrSerSerValGluGlyLeu 200
DB 541 GGAGCCCTGAAATATTAATTCACAAATTAATTCATGCACTTCTGAGAGAGACTT 600

QY 201 CysGlnGlyIleGlyAlaGlyLeuValAspValAlaIleTyrValGlyThrCysSerAsp 220
DB 601 TGTGAAGAAATGTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 660

QY 221 TyrProLysGlyAspAlaSerThrGlyTyrAsnSerValSerArgIleIleIleGlu 240
DB 661 TACCAAAAAGAGAGTCTTCTACTGATGAGATTCAGTTTCGCGATCATTAATGAAGA 720

QY 241 LeuProLys 243
DB 721 CTACCAAAA 729

RESULT 8
ABV99145
ID ABV99145 standard; cDNA; 837 BP.
XX
AC ABV99145;
XX
DT 14-JAN-2003 (first entry)
XX
DE Human pancreatic cancer expressed cDNA SEQ ID NO 4557.
XX
XX
KM Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;
XX
KM cytosolic; tumour; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200260317-A2.
XX
PD 08-AUG-2002.
XX
PF 30-JAN-2002; 2002WO-US002781.
XX
PR 30-JAN-2001; 2001US-0265305P.
XX
PR 31-JAN-2001; 2001US-0265682P.
XX
PR 09-FEB-2001; 2001US-0267568P.
XX
PR 21-MAR-2001; 2001US-0276551P.
XX
PR 28-APR-2001; 2001US-0287112P.

PR 16-MAY-2001; 2001US-0291631P.
 PR 12-JUL-2001; 2001US-0305484P.
 PR 20-AUG-2001; 2001US-0313999P.
 PR 27-NOV-2001; 2001US-0333626P.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Benson DR, Kalos MD, Lodes MJ, Persing DH, Hepler WT, Jiang Y;
 XX WPI; 2002-627435/67.
 DR P-PSDB; ABP66637.
 XX
 PT New isolated polynucleotide and pancreatic tumor polypeptides, useful for
 PT diagnosing, preventing and/or treating cancer, particularly pancreatic
 PT cancer.
 XX
 XX Example 11; SEQ ID NO 4557; 300pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated polynucleotide (1) comprising: (a)
 CC any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b)
 CC complements of (a); (c) sequences consisting of at least 20 contiguous
 CC residues of (a); (d) sequences that hybridize to (a), under moderately
 CC stringent conditions; (e) sequences having at least 75% or 90% identity
 CC to (a); or (f) degenerate variants of (a). Polypeptides (ABP66596-
 CC ABP66637) encoded by (1) and oligonucleotide can be used to detect cancer
 CC in a patient and compositions comprising polypeptides, polynucleotides,
 CC antibodies, fusion proteins, T cell populations and antigen presenting
 CC cells expressing the polypeptide are useful in treating pancreatic cancer
 CC and stimulating an immune response. The polynucleotides can be used as
 CC probes or primers for nucleic acid hybridisation, in the design and
 CC preparation of ribozyme molecules for inhibiting expression of the tumour
 CC polypeptides and proteins in the tumour cells, in vaccines and for gene
 CC therapy. Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pot_sequences
 XX
 SQ Sequence 837 BP; 195 A; 207 C; 238 G; 197 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1.53e-104 Length: 837
 Score: 1301.00 Matches: 243
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: Gaps: 0
 US-10-063-734-122 (1-243) x ABV99145 (1-837)
 QY 1 MetArgProGInGlyProAlaAlaSerProGInArgLeuArgGlyLeuLeuLeuLeu 20
 Db 106 ATGCGACCCCGAGGCGCCCGCCGCTCCCGACGCGGCTCCGCGCTCTGCTCTG 165
 QY 21 LeuLeuGInLeuProAlaProSerSerAlaSerGluLeuProGlyGlyLeuGlnLeuAla 40
 Db 166 CTGCTGCGAGCTCCCGCCGCGCTGAGCTCTGAGTCCCAAGGAGGAGCAAAAGCG 225
 QY 41 GlnLeuArgGlnArgGlnValAlaAspLeuTyrAsnGlyMetCysLeuGlnGlyProAla 60
 Db 226 CAGCTCCGCGAGAGGAGGAGTGTGAGCTGTATATGAAATGTGTTACAAAGGCGCAGCA 285
 QY 61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
 Db 286 GGAAGTGCCTGTGTCAGACGAGGAGCCCTGGGCCCATATGTTATCCGGGTACACCTGGATC 345
 QY 81 ProGlyArgAspGlyPheLeuGlyGlnLeuGlyGlnCysLeuArgGlnLeuGlnGlu 100
 Db 346 CCAAGTCCGAGTGAATTCATAAGAGAGAGAAAGGAGAAAGTCTGAGAGAAAGCTTTGAGAG 405
 QY 101 SerTyrThrProAsnTyrGlnCysSerTyrSerSerLeuAsnTyrGlyIleAspLeu 120
 Db 406 TCCGTGACACCACTCAAGCACTGTTCATGAGGTTCAATTGATTTATGGCATAGATCTT 465
 QY 121 GlyValIleAlaGluCysThrPheThrLysMetArgSerAsnSerAlaLeuArgValLeu 140

Db 466 GGGAAATTCGCGAGATGTACATTTACAAAGATGGCTCAATAGTGTCTAAGATTG 525
 QY 141 PheSerGlySerLeuArgLeuLeuGlySerValArgSerAlaCysCysGlnArgTyrPheThr 160
 Db 526 TTCAGTGGCTTCACTTGGCTTAAATGAGAAATCAATGCTGTCAGCCTTGTGATTCACA 585
 QY 161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGlnAlaIleIleTyrLeuAspGln 180
 Db 586 TTCATGAGAGCTGATGTTGACAGACCTTCCATTACATTAATTTATTGGACCAA 645
 QY 181 GlySerProGlnMetArgSerThrIleAsnIleHisArgThrSerSerValGlnGlyLeu 200
 Db 646 GGAAGCCCTGAAATGAATTCACAAATTAATTCATGCACTTCTGCGAAGGAGACTT 705
 QY 201 CysGlnGlyIleGlyAlaGlyLeuValAspValAlaIleTyrValGlyThrCysSerArg 220
 Db 706 TGTGAAGGAATTTGGTGGCTGATTTAGTGAATGTTGCTACTGCTGCTGCTGCTGAT 765
 QY 221 TyrProGlyGlyAspAlaSerThrGlyTyrAsnSerValSerArgIleIleGlnGlu 240
 Db 766 TACCCAAAGAGATGCTTCTACTGATGATGATGATTCAGTTCTCGCATCATTTAGAGA 825
 QY 241 LeuProGly 243
 Db 826 CTACCAAAA 834
 RESULT 9
 ABS64030
 ID ABS64030 standard; cDNA; 837 BP.
 XX
 XX ABS64030;
 AC
 XX 15-NOV-2002 (first entry)
 DT
 XX
 DE Human breast tumour polynucleotide #479.
 XX
 XX Human, breast tumour protein, gene, ss; breast cancer; cytostatic;
 KW vaccine.
 XX
 XX Homo sapiens.
 OS
 XX US2002085998-A1.
 EN
 XX 04-JUL-2002.
 PD
 XX
 XX 13-APR-2001; 2001US-00834759.
 PF
 XX 28-DEC-1998; 98US-00222575.
 PR 02-APR-1999; 99US-00285480.
 PR 23-JUN-1999; 99US-00339338.
 PR 02-SEP-1999; 99US-00389681.
 PR 03-NOV-1999; 99US-00433826.
 PR 17-APR-2000; 2000US-00551621.
 PR 08-JUN-2000; 2000US-00590751.
 PR 22-JUN-2000; 2000US-00604287.
 PR 20-JUL-2000; 2000US-00620405.
 PR
 XX
 XX (CORI-) CORIXA CORP.
 PA
 XX
 PI Jiang Y, Dillon DC, Mitcham JL, Xu J, Harlocker SL, Hepler WT;
 PI Henderson RA;
 XX
 XX WPI; 2002-635657/68.
 DR P-PSDB; ABG78939.
 XX
 PT Novel breast cancer polynucleotides and polypeptides encoded by the
 PT polynucleotides, useful for detecting the presence of breast cancer in a
 PT patient, and in pharmaceutical compositions, for treating breast cancer.
 XX
 PS Claim 1; Page 234-235; 247pp; English.
 XX
 CC The invention relates to an isolated breast tumour polynucleotide and the

CC polypeptide it encodes. The polynucleotide and polypeptide are useful for
 CC detecting the presence of breast cancer in a patient, and in
 CC pharmaceutical compositions for treating breast cancer. The sequences are
 CC useful for stimulating an immune response in a patient and can therefore
 CC be used in production of vaccines. The sequences are also useful for
 CC detecting the presence of a cancer in a patient, by obtaining a
 CC biological sample from the patient, contacting the biological sample with
 CC a composition of the invention and detecting the amount of polynucleotide
 CC that hybridizes to the sample. This sequence represents a human breast
 CC tumour polynucleotide of the invention

XX Sequence 837 BP; 195 A; 207 C; 238 G; 197 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1,53e-104	Length:	837
Score:	1301.00	Matches:	243
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-10-063-734-122 (1-243) x ABS64030 (1-837)

QY 1 MetArgProGlnGlyProAlaAspProGlnArgLeuArgGlyLeuLeuLeuLeu 20
 DB 106 ATGCGACCCCGAGGGCCCGCCGCCGCCGACGGGCTCCGGGCGCTCGTCTCTCTG 165
 QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluLeuProGlyGlyGlnVal 40
 DB 166 CTGCTTCAGATGCGCCGCGCTGAGGCGCTCTGAGATCCCAAGGGGAAAGCGGCG 225
 QY 41 GlnLeuArgGlnArgGlnValValAspLeuTyrAsnGlyMetCysLeuGlnGlyProAla 60
 DB 226 CAGCTCCGGGAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 285
 QY 61 GlyValProGlyValArgAspGlySerProGlyAlaAsnValLeuProGlyTyrProGlyIle 80
 DB 286 GAGAGTCCTGCTGAGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 345
 QY 81 ProGlyValArgAspGlyPheLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100
 DB 346 CCGAGTCGCGGATGATTCAGAAAGAGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAG 405
 QY 101 SerTyrThrProAsnTyrIleGlnCysSerTyrSerSerLeuAsnTyrGlyIleAspLeu 120
 DB 406 TCTTGGACACCCCACTACAGAGAGTTCATGAGATTCATTGAATTTGCAATGATCTT 465
 QY 121 GlyLeuIleAlaGluCysThrPheThrIleMetArgSerAsnSerAlaLeuArgValLeu 140
 DB 466 GCGAAATTCGCGAGTGTACATTACAAAGATCGTTCAAAATGCTCTTAAGAGTTTTC 525
 QY 141 PheSerGlySerLeuArgLeuLeuValArgAsnAlaCysGlnGlnArgTyrPheThr 160
 DB 526 TTCAGTGGCTCATTGCGCTAAATATGAGAAATGATGCTGATGAGGCTTGATTTTCA 585
 QY 161 PheAsnGlyValAlaGluCysSerGlyProLeuProIleGlnAlaIleLeuTyrLeuAspGln 180
 DB 586 TTCAAATGAGACTAAATGTTGAGAGCTCTTCCATTGAACTTAATTTATTTGAGCAA 645
 QY 181 GlySerProGlnLeuMetArgSerThrIleAsnIleMetArgSerSerValGluGlyLeu 200
 DB 646 GAGAGCCCTGAAATGATTCACAAATTAATTCATGCGCTCTCTGAGAGAGACTT 705
 QY 201 CysGlnGlyTyrIleGlyAlaGlyLeuValAspValAlaIleTyrValGlyTyrCysSerAsp 220
 DB 706 TGTGAAGGATTTGCTGCTGATGATGAGATGTTGCTATCGGCTTGCGCATTTTCAAT 765
 QY 221 TyrProGlyValAspAlaSerThrGlyTyrAsnSerValSerArgIleIleIleGluGln 240
 DB 766 TACCCAAAGGAAATGCTTCTACTGAGTGAATTCAGTTTCTGCGCATTAATTAGAGAA 825
 QY 241 LeuProGly 243
 |||||

DB 826 CTACCAAAA 834

RESULT 10

ABS64031

ID ABS64031 standard; cDNA, 837 BP.

XX ABS64031;

DT 15-NOV-2002 (first entry)

DE Human breast tumour polynucleotide #480.

KW Human; breast tumour protein; gene; ss; breast cancer; cytostatic;

KM vaccine.

XX Homo sapiens.

PN US2002085998-A1.

PD 04-JUL-2002.

PF 13-APR-2001; 2001US-00834759.

PR 28-DEC-1998; 98US-00222575.

PR 02-APR-1999; 99US-00285480.

PR 23-JUN-1999; 99US-00339338.

PR 02-SEP-1999; 99US-00389681.

PR 03-NOV-1999; 99US-00433826.

PR 17-APR-2000; 2000US-00551621.

PR 08-JUN-2000; 2000US-00590751.

PR 22-JUN-2000; 2000US-00604287.

PR 20-JUL-2000; 2000US-00620405.

XX (CORI-) CORIAX CORP.

XX Jiang Y, Dillon DC, Mitcham JL, Xu J, Harlocker SL, Hepler WT;

PI Henderson RA;

XX WPI; 2002-635657/68.

DR P-PSDB; ABG78939.

XX Novel breast cancer polynucleotides and polypeptides encoded by the

PT polynucleotides, useful for detecting the presence of breast cancer in a

PT patient, and in pharmaceutical compositions, for treating breast cancer.

XX Claim 1; Page 235; 247pp; English.

XX The invention relates to an isolated breast tumour polynucleotide and the

CC polypeptide it encodes. The polynucleotide and polypeptide are useful for

CC detecting the presence of breast cancer in a patient, and in

CC pharmaceutical compositions for treating breast cancer. The sequences are

CC useful for stimulating an immune response in a patient and can therefore

CC be used in production of vaccines. The sequences are also useful for

CC detecting the presence of a cancer in a patient, by obtaining a

CC biological sample from the patient, contacting the biological sample with

CC a composition of the invention and detecting the amount of polynucleotide

CC that hybridizes to the sample. This sequence represents a human breast

CC tumour polynucleotide of the invention

XX Sequence 837 BP; 195 A; 207 C; 238 G; 197 T; 0 U; 0 Other;

XX Alignment Scores:

Pred. No.:	1,53e-104	Length:	837
Score:	1301.00	Matches:	243
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-10-063-734-122 (1-243) x ABS64031 (1-837)

QY 1 MetArgProGlnGlyProAlaAspProGlnArgLeuArgGlyLeuLeuLeuLeu 20
 |||||

Db 106 ATGCAACCCAGGCGCCGCCCTCCCGCAGCGGCTCCGGGCTCTGCTGCTCCG 165
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluLeuProGlyGlyGlnVala 40
Db 166 CTGCTGACAGCTGCCCGCCGCTGAGCGCTCTGAGATCCCAAGGAGGAAAGGCG 225
QY 41 GlnLeuArgGlnArgGluValaValaLeuLeuTyrAanglyMetCysLeuGlnGlyProAla 60
Db 226 CAGCTCCGCGAGAGGAGGTGTGAGCTGTATATGAAATGTGCTTCAAGGGGCGCA 285
QY 61 GlyValProGlyArgAspGlySerProGlyAlaAenValleleProGlyThrProGlyTle 80
Db 286 GAGAGTCTGTGTCAGAGCGAGGAGCCCTGGGCTCAATGTATTCGGGTACACCTGGGATC 345
QY 81 ProGlyArgAspGlyPheGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100
Db 346 CCAAGTCCGAGTGTCAAAAGAGAAAGGGGAGATCTCGAGGAAAGCTTTGAGAG 405
QY 101 SerTrpThrProAsnTyrLeuGlnCysSerTrpSerSerLeuAenTyrGlyTleAspLeu 120
Db 406 TCCGTGACACCCCACTACAGACAGTGTCAATGAGTTCATTGAAATTAATGCAATGATCTT 465
QY 121 GlyValleuAlaGlyCysThrPheThrLysMetArgSerAenSerAlaLeuArgValleu 140
Db 466 GGGAAATTCGCGAGTGTACATTACAAAGATGCGCTCAATTAAGTCTTAAAGTTTG 525
QY 141 PheSerGlySerLeuArgLeuGlyCysArgAsnAlaCysCysGlnArgTyrPheThr 160
Db 526 TTCAGTGTCTCTGCTCGCTAAATGCAAAATGCAATGCTGCTGCTGCTGCTGCTGCTG 585
QY 161 PheAsnGlyAlaGlyCysSerGlyProLeuProGlnAlaLeuLeuLeuLeuLeuLeu 180
Db 586 TTCATATGAGCTGATGTTCAGGACCTCTCCATTAACCTTAATTAATTAATTAATTAAT 645
QY 181 GlySerProGlnMetAenSerThrTleAsnTleHisArgThrSerSerValGlnGlyLeu 200
Db 646 GGAAGCCCTGAAATGATTCACAAATTAATTAATTAATTAATTAATTAATTAATTAAT 705
QY 201 CysGlnGlyTleGlyAlaGlyLeuValaAspValaAlleleThrValaGlyThrCysSerAsp 220
Db 706 TGTGAAGGATTTGCTGCTGATTAAGTGTGATTTGCTGATTTGCTGATTTGCTGATTTG 765
QY 221 TyrProGlyGlyAspAlaSerThrGlyTyrPAsnSerValSerArgTleTleGlnGly 240
Db 766 TACCCCAAGAGATGCTTCTACTGATGATGAAATTCAGTTTTCGCAATCAATTGTAAGA 825
QY 241 LeuProGly 243
Db 826 CTACCAAAA 834
RESULT 11
ABT33242
ID ABT33242 standard; DNA; 837 BP.
XX
AC ABT33242;
XX
DT 15-MAY-2003 (first entry)
XX
DB Human tumour-related DNA sequence - SEQ ID No 512.
XX
KW Human; ds; vaccine; gene therapy; T cell stimulation; T cell expansion;
KW tumour; breast cancer; cancer; immune response stimulation.
XX
OS Homo sapiens.
XX
PN W0200283956-A1.
XX
PD 24-OCT-2002.
XX
PF 15-APR-2002; 2002WO-US012378.
XX
PR 13-APR-2001; 2001US-00834759.
PR 07-DEC-2001; 2001US-00007805.

PR 13-FEB-2002; 2002US-00076622.
XX
XX (CORI-) CORIXA CORP.
XX
PI Houghton RL, Sleath PR, Persing DH, Jiang Y, Dillon DC,
PI Mitcham JL, Xu J, Harlocke SL, Hepler WT, Henderson RA, Fanger GR,
PI Vedvick TS, McNeill PD, Durham M,
XX WPI; 2003-103376/09.
XX
XX New polypeptide and polynucleotide useful for stimulating and/or
PT expanding T cells specific for a tumor protein and treating breast
PT cancer.
XX
XX Example 1; Page 320; 375pp; English.
XX
CC The invention, comprises a method of stimulating and/or expanding T cells
CC specific for a tumor protein. The invention further comprises human
CC nucleic acids and proteins that are associated with tumors (e.g. breast
CC cancer). The method and sequences of the invention are useful for
CC stimulating and/or expanding T cells specific for a tumor protein,
CC detecting the presence of cancer, stimulating an immune response in a
CC patient and treating breast cancer. The present DNA sequence represents a
XX human tumour-related DNA sequence
XX
SQ Sequence 837 BP; 195 A; 207 C; 238 G; 197 T; 0 U; 0 Other;
Alignment Scores:
Score: 1.53e-104 Length: 837
Percent Similarity: 1301.00 Matches: 243
Best Local Similarity: 100.00% Conservative: 0
Query Match: 100.00% Mismatches: 0
DB: 10 Indels: 0 Gaps: 0
US-10-063-734-122 (1-243) x ABT33242 (1-837)
QY 1 MetArgProGlnGlyProAlaAspProGlnArgLeuArgGlyLeuLeuLeuLeu 20
Db 106 ATGCAACCCAGGCGCCGCCCTCCCGCAGCGGCTCCGGGCTCTGCTGCTCCG 165
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluLeuProGlyGlyGlnVala 40
Db 166 CTGCTGACAGCTGCCCGCCGCTGAGCGCTCTGAGATCCCAAGGAGGAAAGGCG 225
QY 41 GlnLeuArgGlnArgGluValaValaLeuLeuTyrAanglyMetCysLeuGlnGlyProAla 60
Db 226 CAGCTCCGCGAGAGGAGGTGTGAGCTGTATATGAAATGTGCTTCAAGGGGCGCA 285
QY 61 GlyValProGlyArgAspGlySerProGlyAlaAenValleleProGlyThrProGlyTle 80
Db 286 GAGAGTCTGTGTCAGAGCGAGGAGCCCTGGGCTCAATGTATTCGGGTACACCTGGGATC 345
QY 81 ProGlyArgAspGlyPheGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100
Db 346 CCAAGTCCGAGTGTCAAAAGAGAAAGGGGAGATCTCGAGGAAAGCTTTGAGAG 405
QY 101 SerTrpThrProAsnTyrLeuGlnCysSerTrpSerSerLeuAenTyrGlyTleAspLeu 120
Db 406 TCCGTGACACCCCACTACAGACAGTGTCAATGAGTTCATTGAAATTAATGCAATGATCTT 465
QY 121 GlyValleuAlaGlyCysThrPheThrLysMetArgSerAenSerAlaLeuArgValleu 140
Db 466 GGGAAATTCGCGAGTGTACATTACAAAGATGCGCTCAATTAAGTCTTAAAGTTTG 525
QY 141 PheSerGlySerLeuArgLeuGlyCysArgAsnAlaCysCysGlnArgTyrPheThr 160
Db 526 TTCAGTGTCTCTGCTCGCTAAATGCAAAATGCAATGCTGCTGCTGCTGCTGCTGCTG 585
QY 161 PheAsnGlyAlaGlyCysSerGlyProLeuProGlnAlaLeuLeuLeuLeuLeuLeu 180
Db 586 TTCATATGAGCTGATGTTCAGGACCTCTCCATTAACCTTAATTAATTAATTAATTAAT 645

QY 181 GlySerProGluMeAsnSerThrIleAsnIleHisArgThrSerSerValGluGluLeu 200
DB 646 GGAAGCCCTGAAATGATTCACAAATTATTCATCGCACTTCTCTGGAGAGACTT 705
QY 201 CysGluGlyIleGlyValaGlyLeuValaIleIleTrpValGlyThrCysSerAsp 220
DB 706 TGTGAAGGAATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 765
QY 221 TyrProLysGlyAspAlaSerThrGlyTrpAsnSerValSerArgIleIleIleGluGlu 240
DB 766 TACCCAAAGAGAGATGCTTCTACTGATGAGATTCAGTTCTCGCAATCATTTGAAGA 825
QY 241 LeuProLys 243
DB 826 CTACCAAAA 834
RESULT 12
ABT33243
ID ABT33243 standard; DNA; 837 BP.
XX ABT33243;
AC
XX
XX 15-MAY-2003 (first entry)
DE Human tumour-related DNA sequence - SEQ ID NO 513.
XX
XX Human; ds; vaccine; gene therapy; T cell stimulation; T cell expansion;
KM tumour; breast cancer; cancer; immune response stimulation.
XX Homo sapiens.
XX WO200283956-A1.
XX 24-OCT-2002.
XX 15-APR-2002; 2002WO-US012378.
XX 13-APR-2001; 2001US-00834759.
PR 07-DEC-2001; 2001US-00007805.
PR 13-FEB-2002; 2002US-00076622.
XX
XX (CORI-) CORIXA CORP.
XX Houghton RL, Sleath PR, Persing DH, Jiang Y, Dillon DC;
PI Mitcham JL, Xu J, Harlocker SL, Hepler WT, Henderson RA, Fanger GR;
PI Vedvick TS, McNeill PD, Durham M;
XX
XX WPI; 2003-103376/09.
XX
XX New polypeptide and polynucleotide useful for stimulating and/or
PT expanding T cells specific for a tumor protein and treating breast
PT cancer.
XX
XX Example 1; Page 321; 375pp; English.
XX
XX The invention comprises a method of stimulating and/or expanding T cells
CC specific for a tumour protein. The invention further comprises human
CC nucleic acids and proteins that are associated with tumours (e.g. breast
CC cancer). The method and sequences of the invention are useful for
CC stimulating and/or expanding T cells specific for a tumour protein,
CC detecting the presence of cancer, stimulating an immune response in a
CC patient and treating breast cancer. The present DNA sequence represents a
CC human tumour-related DNA sequence
XX
XX Sequence 837 BP; 195 A; 207 C; 238 G; 197 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 1.53e-104 length: 837
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-063-734-122 (1-243) x ABT33243 (1-837)
QY 1 MetArgProGlnGlyProAlaIleAspProGlnArgLeuArgGlyLeuLeuLeuLeu 20
DB 106 ATGCGACCCCGAGGGCCGCCCTCCCGCAGCGGCTCCGGGCTCTGCTGCTCTG 165
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluIleProLysGlyLysGlnVala 40
DB 166 CTGCTGCACTGCGCCCGCCGCTGAGCGCTCTGAGATCCCAAGGAGAAAGAGCGC 225
QY 41 GlnLeuArgGlnArgGluValaIleAspLeuTyrAsnGlyMetCysLeuGlnGlyProAla 60
DB 226 CAGCTCCGCGAGGGAGGTGGTGGAGCTGTATATGGAATGCTTACAAAGGCGCAGCA 285
QY 61 GlyValProGlyValArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
DB 286 GAGATGCTGCTGCGAGACCGGAGCCCTGGGGCCAAATGTTATCCGGGTACCTGGGATC 345
QY 81 ProGlyValArgAspGlyPheLysGlyGlyValGlyCysLeuArgGlyLysSerPheGluGlu 100
DB 346 CCAAGTCGGAGATGATTCAAAGAGAGAAAGGGGAAATGCTGAAGGAAAGCTTTGAGAG 405
QY 101 SerTrpThrProAsnTyrLysGlnCysSerTrpSerSerLeuAsnTyrGlyIleAspLeu 120
DB 406 TCCTGGACACCCCACTACAAAGCAGTGTTCATGAGATTGATGATGATGATGATGAT 465
QY 121 GlyLysIleAlaGluCysThrPheThrLysMetArgSerAsnSerAlaLeuArgValLeu 140
DB 466 GGGAAATATGCGAGGTGATCATTTACAAAGATGCGTTCAAAATAGTCTCTAAGAGCTTTG 525
QY 141 PheSerGlySerLeuArgLeuLysCysArgAsnAlaCysCysGluArgTrpTyrPheThr 160
DB 526 TTCAGTGCTCACTTCGCTCAAAATGCAAGAAATGCAATGCTGTCAGGCTTGATTTCACA 585
QY 161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleTyrLeuAspGln 180
DB 586 TTCAAATGAGAGCTGATGATTCAGGACCTCTCCCATTTGAAGCATATATTATTGACCAA 645
QY 181 GlySerProGluMeAsnSerThrIleAsnIleHisArgThrSerSerValGluGluLeu 200
DB 646 GGAAGCCCTGAAATGATTCACAAATTATTCATTCGCACTTCTCTGGAGAGACTT 705
QY 201 CysGluGlyIleGlyValaGlyLeuValaIleIleTrpValGlyThrCysSerAsp 220
DB 706 TGTGAAGGAATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 765
QY 221 TyrProLysGlyAspAlaSerThrGlyTrpAsnSerValSerArgIleIleIleGluGlu 240
DB 766 TACCCAAAGAGAGATGCTTCTACTGATGAGATTCAGTTCTCGCAATCATTTGAAGA 825
QY 241 LeuProLys 243
DB 826 CTACCAAAA 834
RESULT 13
ADL93174
ID ADL93174 standard; cDNA; 837 BP.
XX
XX ADL93174;
AC
XX
XX 20-MAY-2004 (first entry)
DT
XX
XX Human breast cancer-associated polypeptide cDNA #476.
DE
XX
XX gene therapy; protein therapy; vaccine; breast cancer; cancer; human; ss;
KM gene.
XX
XX Homo sapiens.
OS
XX
XX US2003166022-A1.
PN
XX
XX 04-SEP-2003.
PD

XX 15-APR-2002; 2002US-00124805.
 PF 28-DEC-1998; 98US-00222575.
 PR 02-APR-1999; 99US-00285480.
 PR 23-JUN-1999; 99US-00339338.
 PR 02-SEP-1999; 99US-00389681.
 PR 03-NOV-1999; 99US-00433826.
 PR 17-APR-2000; 2000US-00551621.
 PR 08-JUN-2000; 2000US-00590751.
 PR 22-JUN-2000; 2000US-00604287.
 PR 20-JUL-2000; 2000US-00620405.
 PR 13-APR-2001; 2001US-00834759.
 PR 07-DEC-2001; 2001US-00007805.
 PR 13-FEB-2002; 2002US-00076622.
 XX (CORI-) CORIXA CORP.
 PA Houghton RL, Sleath PR, Persing DH;
 PI WPI, 2003-874918/81.
 DR P-PSDB; ADL93177.
 DR
 XX
 XX An isolated oncogenic polypeptide useful for preventing, diagnosing and
 PT treating breast cancer.
 PS Example 1; SEQ ID NO 512; 294pp; English.
 CC The invention relates to an isolated breast cancer-associated
 CC polypeptide. The polypeptide may be used for the diagnosis and treatment
 CC of breast cancers. The methods are useful for detecting the presence of a
 CC cancer in a patient and treating a cancer in a patient. The present
 CC sequence represents cDNA encoding a human breast cancer-associated
 CC polypeptide.
 XX
 SQ Sequence 837 BP; 195 A; 207 C; 238 G; 197 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1 53e-104 Length: 837
 Score: 1301.00 Matches: 243
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 11 Gaps: 0
 US-10-063-734-122 (1-243) x ADL93174 (1-837)
 QY 1 MetAgtPProGlnGlyProAlaAlaSerProGlnArgGlyLeuLeuLeuLeu 20
 DB 106 ATGCGACCCCAAGGCGCCCGCTCCCGCAGCGGCTCCGCTCTGCTCTG 165
 QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluLeuProGlyGlyLeuGln 40
 DB 166 CTGCTGCAAGCTGCGCGCGCTGAGCGCTGAGATCCCAAGGGAAGCAAAAGCG 225
 QY 41 GlnLeuArgGlnArgGlnValValAspLeuTyrAsnGlyMetCysLeuGlnGlyProAla 60
 DB 226 CAGCTCCCGCAGAGGAGGAGTGTGACCTGTAATGAAATGCTTCAAGAGGCAACA 285
 QY 61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyTyr 80
 DB 286 GGAAGTCTGTGTCAGACGAGGAGCCCTGGGCGCATGTTATTCGGGTACACCTGGGATC 345
 QY 81 ProGlyArgAspGlyPheLeuGlyGlyValGlyGlyGlyCysLeuArgGlySerPheGluGlu 100
 DB 346 CCAAGTGGGAGTGAATCAAGAGAGAAAGGGAGATGTCTGAGGAAAGCTTTGAGAGAG 405
 QY 101 SerThrProAsnTyrLeuGlnCysSerTyrSerSerLeuAsnTyrGlyTyrLeuAspLeu 120
 DB 406 TCCCTGACACCACTCAACAGACGTTCATGAGTTCATTTGATTAATGCAATGATCTT 465
 QY 121 GlyValIleAlaGluCysThrPheThrIleMetArgSerAsnSerAlaLeuArgValLeu 140

DB 466 GGGAAATTCGAGTGTACATTTACAAAGATGCGCTCAATAGTGTCAAGATTG 525
 QY 141 PheSerGlySerLeuArgLeuLeuYsCysArgAsnAlaCysGlnArgTyrPheThr 160
 DB 526 TTCAGTGGCTCACTTCGGCTAAATGACAGAAATGATGCTGAGCGTGTGATTCACA 585
 QY 161 PheArgGlyAlaGluCysSerGlyProLeuProIleGluAlaIleTyrLeuAspGln 180
 DB 586 TTCATGAGCTGATGATGTTACAGACCTTCCATTTAGAGCTAAATTTATTTGACCAA 645
 QY 181 GlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGluGlyLeu 200
 DB 646 GGAAGCCCTGAATATTAATCAACATTAATTCATGACACTTCTGTGGAAGACCTT 705
 QY 201 CysGluGlyIleGlyAlaGlyLeuValAspValAlaIleTyrValGlyThrCysSerAsp 220
 DB 706 TGTGAAGGATTTGGTGTGATTTAGTGTGATTTCTGCTGCTGCTGCTGCTGCTGAT 765
 QY 221 TyrProGlyGlyAspAlaSerThrGlyTyrAsnSerValSerArgIleIleIleGluGln 240
 DB 766 TACCCAAAGAGATGCTTCTTAATGATGATGATGATGATGATGATGATGATGATGAT 825
 QY 241 LeuProLys 243
 DB 826 CTACCAAAA 834
 RESULT 14
 ADL93175
 ID ADL93175 standard; cDNA; 837 BP.
 XX
 AC ADL93175;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Human breast cancer-associated polypeptide cDNA #477.
 XX
 KW gene therapy; protein therapy; vaccine; breast cancer; cancer; human; ss;
 KW gene.
 XX
 OS Homo sapiens.
 XX
 FN US2003166022-A1.
 XX
 PD 04-SEP-2003.
 XX
 PF 15-APR-2002; 2002US-00124805.
 XX
 PR 28-DEC-1998; 98US-00222575.
 PR 02-APR-1999; 99US-00285480.
 PR 23-JUN-1999; 99US-00339338.
 PR 02-SEP-1999; 99US-00389681.
 PR 03-NOV-1999; 99US-00433826.
 PR 17-APR-2000; 2000US-00551621.
 PR 08-JUN-2000; 2000US-00590751.
 PR 22-JUN-2000; 2000US-00604287.
 PR 20-JUL-2000; 2000US-00620405.
 PR 13-APR-2001; 2001US-00834759.
 PR 07-DEC-2001; 2001US-00007805.
 PR 13-FEB-2002; 2002US-00076622.
 XX
 PA (CORI-) CORIXA CORP.
 PI Houghton RL, Sleath PR, Persing DH;
 DR WPI, 2003-874918/81.
 DR
 XX
 XX An isolated oncogenic polypeptide useful for preventing, diagnosing and
 PT treating breast cancer.
 PS Example 1; SEQ ID NO 513; 294pp; English.
 CC The invention relates to an isolated breast cancer-associated
 CC polypeptide. The polypeptide may be used for the diagnosis and treatment

CC of breast cancers. The methods are useful for detecting the presence of a
 CC cancer in a patient and treating a cancer in a patient. The present
 CC sequence represents cDNA encoding a human breast cancer-associated
 CC polypeptide.

XX SQ Sequence 837 BP; 195 A; 207 C; 238 G; 197 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1 53e-104	Length:	837
Score:	1301.00	Matches:	243
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	11	Gaps:	0

US-10-063-734-122 (1-243) x ADB93175 (1-837)

```

QY 1 MetArgProGlnGlyProAlaIaIaSerProGlnArgLeuArgGlyLeuLeuLeu 20
DB 106 ATGCCAGCCCGAGGGCCCGCCCTCCCGCAGCGGCTCCGCGCTCTGCTCTCTG 165
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluIleProLysGlyLysGlnYsAla 40
DB 166 CTGCTGCACAGTCCCGCCGCGCTGAGCGCTCTGAGATCCCAAGGGGAAAGAGCG 225
QY 41 GlnLeuArgGlnArgGluValValAspLeuTyrAsnGlyMetCysLeuGlnGlyProAla 60
DB 226 CAGCTCCGGAGAGGAGGTGTGACCTGTATTAAGAAATGTCTTACAGGCGCAGCA 285
QY 61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
DB 286 GGAGTCCCTGCTGAGACCGGAGCCCTGGGCGCAATGTTATTCGGGTACACCTGGGATC 345
QY 81 ProGlyArgAspGlyPheLysGlyLysGlyGlyCysLeuArgGlyLysSerPheGln 100
DB 346 CCAGGTCCGGATGATTCAGAAAGAGAAAGGGGGAATGTCTGAGGAAAGCTTGAAGAG 405
QY 101 SerTrpThrProAsnTyrLysGlnCysSerTrpSerLeuAsnTyrGlyIleAspLeu 120
DB 406 TCTTGACACCCCACTACACAGCTGTCTGAGATTCATTGATTAATGATGATGATCTT 465
QY 121 GlyLysIleAlaGlnCysThrPheThrLysMetArgSerAsnSerAlaLeuArgValLeu 140
DB 466 GGGAAATATTCGAGAGTACATTATTAACAAGATCCGTTCAATATGCTCTTAAGATTTTG 525
QY 141 PheSerGlySerLeuArgLeuLysCysArgAsnAlaCysCysGlnArgTyrPheThr 160
DB 526 TTCAGTGGCTCACTTCGCTAAATATGACAAATGATGATGCTGACGCTGTATTCACA 585
QY 161 PheAsnGlyAlaGlnCysSerGlyProLeuProIleGlnAlaIleIleTyrLeuAspGln 180
DB 586 TTCAAATGAGAGTGAATGTCAAGACCTCTCCATTAAGCTTAATTAATTTGAAGCA 645
QY 181 GlySerProGlnMetAsnSerThrIleAsnIleHisArgThrSerSerValGlnGlyLeu 200
DB 646 GGAAGCCCTGAAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 705
QY 201 CysGlnGlyIleGlyAlaGlyLeuValAspValAlaIleTyrValGlyLysSerAsp 220
DB 706 TGTGAAGGAATGTGTCTGATTAAGATGTTGCTATCTGAGGTGGCACTGTTCAGAT 765
QY 221 TyrProLysGlyAspAlaSerThrArgTyrPheAsnSerValSerArgIleIleIleGlnGlu 240
DB 766 TACCCTAAAGAGATCTTCTACTGATGATGAAATTCAGTTCTGCAATCATTAATTAAGA 825
QY 241 LeuProLys 243
DB 826 CTACCAAAA 834

```

RESULT 15
 ADB90997
 ID ADB90997 standard; cDNA; 1256 BP.
 XX

AC ADB90997;
 XX
 DT 04-DEC-2003 (first entry)

DE Novel human secreted and transmembrane protein PRO1550 cDNA.

KW ss; gene; human; PRO; pharmaceutical; diagnostic; biosensor; bioreactor;
 KM affinity purification; secreted and transmembrane protein.

XX Homo sapiens.

XX US2003083473-A1.

XX 01-MAY-2003.

XX 03-MAY-2002; 2002US-00063595.

XX 06-DEC-2001; 2001US-00006867.

XX (GENTH) GENENTECH INC.

PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;

XX WPI; 2003-786922/74.

DR P-PSDB; ADB90998.

PT New antibody that binds a secreted and transmembrane polypeptide (PRO)
 PT for treating cancer and for diagnostic assays and affinity purification

PS of PRO.

XX Disclosure; Fig 121; 408pp; English.

XX The invention describes an antibody that specifically binds to a PRO
 CC polypeptide having a fully defined amino acid sequence given in the

CC specification. The antibody is useful in identifying PRO polypeptides
 CC useful for various industrial applications, including pharmaceuticals,

CC diagnostic, biosensors and bioreactors. The antibody is also used for
 CC affinity purification of PRO polypeptides from recombinant cell culture

CC or natural sources. The antibody, PRO polypeptide, or its agonists or
 CC antagonists, may be used for preparing a medicament for diagnosing or

CC treating a condition responsive to the antibody, PRO polypeptide, or its
 CC agonists or antagonists. This sequence encodes a novel human secreted and

CC transmembrane PRO polypeptide.

XX SQ Sequence 1256 BP; 324 A; 264 C; 299 G; 369 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2 54e-104	Length:	1256
Score:	1301.00	Matches:	243
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-063-734-122 (1-243) x ADB90997 (1-1256)

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DB 138 ATGCCAGCCCGAGGGCCCGCCCTCCCGCAGCGGCTCCGCGCTCTGCTCTCTG 197
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluIleProLysGlyLysGlnYsAla 40
DB 198 CTGCTGCACAGTCCCGCCGCGCTGAGCGCTCTGAGATCCCAAGGGGAAAGAGCG 257
QY 41 GlnLeuArgGlnArgGluValValAspLeuTyrAsnGlyMetCysLeuGlnGlyProAla 60
DB 258 CAGCTCCGGCAGAGGAGGTGTGACCTGTATTAATGAAATGTCTTACAGGCGCAGCA 317
QY 61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
DB 318 GGAGTCCCTGCTGAGACCGGAGCCCTGGGCGCAATGTTATTCGGGTACACCTGGGATC 377

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PR	15-SEP-1998	98US-0100370
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PR	16-SEP-1998	98US-0100631
PR	16-SEP-1998	98US-0100632
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PR	16-SEP-1998	98US-0100634
PR	17-SEP-1998	98US-0100644
PR	17-SEP-1998	98US-0100710
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PR	18-SEP-1998	98US-0100849
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PR	22-SEP-1998	98US-0101279
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PR	23-SEP-1998	98US-0101478
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PR	29-SEP-1998	98US-0102207
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PR	01-OCT-1998	98US-0102684
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PR	06-OCT-1998	98US-0103258
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PR	07-OCT-1998	98US-0103314
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PR	22-OCT-1998	98US-0105266
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PR	27-OCT-1998	98US-0105818
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PR	27-OCT-1998	98US-0106062
PR	28-OCT-1998	98US-0106023

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PR 28-OCT-1998; 98US-0106029P.
PR 28-OCT-1998; 98US-0106030P.
PR 28-OCT-1998; 98US-0106032P.
PR 28-OCT-1998; 98US-0106033P.
PR 28-OCT-1998; 98US-0106178P.
PR 29-OCT-1998; 98US-0106248P.
PR 29-OCT-1998; 98US-0106348P.
PR 29-OCT-1998; 98US-0106500P.
PR 30-OCT-1998; 98US-0106464P.
PR 03-NOV-1998; 98US-0106856P.
PR 03-NOV-1998; 98US-0106902P.
PR 03-NOV-1998; 98US-0106905P.
PR 03-NOV-1998; 98US-0106919P.
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PR 03-NOV-1998; 98US-0106934P.
PR 10-NOV-1998; 98US-0107783P.
PR 17-NOV-1998; 98US-0108775P.
PR 17-NOV-1998; 98US-0108779P.
PR 17-NOV-1998; 98US-0108787P.
PR 17-NOV-1998; 98US-0108788P.
PR 17-NOV-1998; 98US-0108801P.
PR 17-NOV-1998; 98US-0108802P.
PR 17-NOV-1998; 98US-0108806P.
PR 17-NOV-1998; 98US-0108807P.
PR 17-NOV-1998; 98US-0108825P.
PR 18-NOV-1998; 98US-0108848P.
PR 18-NOV-1998; 98US-0108849P.
PR 18-NOV-1998; 98US-0108850P.
PR 18-NOV-1998; 98US-0108851P.
PR 18-NOV-1998; 98US-0108852P.
PR 18-NOV-1998; 98US-0108858P.
PR 18-NOV-1998; 98US-0108904P.
XX
XX (GETH ) GENENTECH INC.
XX
XX Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WT;
XX WPI, 2000-237871/20.
XX P-PSDB; AAY99462.
XX
XX New mammalian DNA sequences encoding transmembrane, receptor or secreted
XX PRO polypeptides, useful for screening of potential peptide or small
XX molecule inhibitors of the relevant receptor/ligand interactions.
XX
XX Claim 2; Fig 245; 773pp; English.
XX
XX AAA37022 to AAA37144 encode the new isolated human transmembrane,
XX receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The
XX transmembrane and receptor PRO proteins can be used for screening of
XX potential peptide or small molecule inhibitors of the relevant
XX receptor/ligand interactions. The polypeptides and nucleotide sequences
XX encoding then have various industrial applications, including uses as
XX pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR
XX primers and hybridisation probes used in the isolation of the PRO
XX polypeptides from the present invention
XX
XX SQ Sequence 1257 BP; 324 A; 264 C; 299 G; 370 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 2 55e-104 length: 1257
XX Score: 1301.00 Matches: 243
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 100.00% Indels: 0
XX DB: 3 Gaps: 0
XX
XX US-10-063-734-122 (1-243) x AAA37144 (1-1257)
XX
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XX |||||
XX DB 138 ATCGACACCCAGGCGCCGCGCTCCCGCACAGGCGCTCGCGGCTCTCGTCTCTCG 197

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QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluIleProTyrGlyLeuGlnVala 40
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QY 41 GlnLeuArgGlnArgGlyValaValaIaIaSerLeuTyrArgGlyMetCysLeuGlnGlyProAla 60
DB CAGCTCCGCGACAGGAGGTGTGTGACCTGTATATGAAATGTGTCTACAAAGGCGCAGCA 317
QY 61 GlyValProGlnValArgArgGlySerProGlyAlaIaIaIleProGlyThrProGlyIle 80
DB GGAGTGCCTGTGACAGCGGAGCCCTGCGGCAATGTATTTCCGGTACACCTTGGAGTC 377
QY 81 ProGlyArgArgGlyPheIleGlyGlnTyrGlyGlyCysLeuArgGlySerPheGlnGln 100
DB CAGGTCCGAGATGATTTCAAGAGAAAGGGGAAATGCTTACAGGAAAGCTTTGAGAG 437
QY 101 SerTrpThrProAsnTyrIleGlyGlnCysSerTrpSerSerLeuAsnTyrGlyIleAspLeu 120
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QY 121 GlyIleIleAlaGluCysThrPheThrIleMetArgSerSerAlaLeuArgValLeu 140
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QY 141 PheSerGlySerLeuArgLeuIleCysArgAsnAlaCysCysGlnArgTrpTrpPheThr 160
DB TTCAGTGGCTCACTTCCTCGCTAAATGCAAAATGCAATGCTGACGCTTGGATTTTACA 617
QY 161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleTyrLeuAspGln 180
DB TTCATATGAGCTGAAATGTTCAAGACCTCTCCCATTTGAAGCATATATTATTGACCA 677
QY 181 GlySerProGluMetAsnSerThrIleAsnIleIleIleIleIleIleIleIleIleIle 200
DB GGAAGCCCTGAATGATTCACCAATTAATTTCAATTCGACCTTCTCTGTGAAGACTT 737
QY 201 CysGlnGlyIleGlyAlaGlyLeuValaIaIaIleTrpValGlyThrCysSerAsp 220
DB TGTGAAGGAAATGTGTGCTGAGATTAATGATGTGCTATCTGAGTTGGCACTTGTCAGAT 797
QY 221 TyrProTyrGlyAspAlaSerThrGlyTyrAsnSerValSerArgIleIleIleGlnGln 240
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QY 241 LeuProTyr 243
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XX RESULT 17
XX AAF54507
XX ID AAF54507 standard; DNA; 1257 BP.
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XX AAF54507;
XX AC
XX DT 02-APR-2001 (first entry)
XX
XX DE Probe #60 used in the identification of proteins.
XX
XX KM Secreted; transmembrane; gene therapy; ss.
XX
XX OS Unidentified.
XX
XX PN WO200078961-A1.
XX
XX PD 28-DEC-2000.
XX
XX PF 18-FEB-2000; 2000MCO-US004342.
XX
XX XX 23-JUN-1999; 99US-0141037P.
XX PR 26-JUL-1999; 99US-0144758P.
XX PR 01-SEP-1999; 99US-0145698P.
XX PR 29-OCT-1999; 99US-0162506P.

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03-MAY-2000; 2000US-0201516P.

17-MAY-2000; 2000WO-US013705.

PR 22-MAY-2000; 2000MO-US014042.
PR 30-MAY-2000; 2000MO-US014941.
PR 02-JUN-2000; 2000MO-US015264.
PR 05-JUN-2000; 2000US-0209832P.
PR 28-JUL-2000; 2000MO-US020710.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000MO-US023328.
PR 08-NOV-2000; 2000MO-US030952.
PR 01-DEC-2000; 2000MO-US032678.
PR 20-DEC-2000; 2000MO-US034956.
XX
XX (GETH) GENENTECH INC.
XX
PI Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX P-PSDB; AAU29206.
XX WPI; 2001-602746/68.
XX
PT Novel nucleic acids encoding PRO polypeptides, used to diagnose the
PT presence of tumors, such as prostate and breast tumors, in mammals and to
PT screen for modulators of the compounds.
XX
XX Claim 2; Fig 365; 774pp; English.
XX
CC Sequences AAS45925-AAS46231 represent DNA molecules encoding and PCR
CC primers for PRO polypeptides of the invention. The sequences of the
CC invention can be used to detect the presence of a tumour in a mammal by
CC comparing the level of expression of a PRO polypeptide in a test sample
CC of cells from the animal and a control sample of normal cells, whereby a
CC higher level of expression in the test sample indicates the presence of a
CC tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep,
CC pigs, goats and rabbits but are preferably human. The polypeptides can be
CC used to stimulate tumour necrosis factor (TNF) alpha release from human
CC blood, when contacted with it. A specific polypeptide can be used to
CC stimulate the proliferation or differentiation of chondrocyte cells. The
CC PRO proteins can be used to determine the presence of tumours and also
CC susceptibility to tumour development, particularly adrenal, lung, colon,
CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC can be used for genetic analysis of individuals with genetic disorders
XX
SQ Sequence 1257 BP; 324 A; 264 C; 299 G; 370 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 2.55e-104 Length: 1257
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
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Db 198 CTGCTCAGCTGCGCGCGCGCTGAGCGCTCTGAGATCCCAAGGGAAGCAAGGGGG 257
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QY 61 GlyValProGlyValArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
Db 318 GAGAGCTCGGTGAGAGCGGAGCCCTGGGCGCAATGTTATTCGGGTACACCTGGGATC 377
QY 81 ProGlyValArgAspGlyPheLeuGlyGlyGlyGluCysLeuArgGlnSerPheGlnGlu 100
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QY 141 PheSerGlySerLeuArgLeuLysCysArgAsnAlaCysCysGlnArgTPTrPheThr 160
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Db 798 TACCCAAAGAGATGCTTCTACTGGATGAATTCAGTTTCGCAATTAATTGAAGAA 857
QY 241 LeuProLys 243
Db 858 CTACCAAA 866
RESULT 19
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ID AAF92118 standard; cDNA; 1257 BP.
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XX AAF92118;
AC 15-MAY-2001 (first entry)
DT
DT 15-MAY-2001 (first entry)
XX
XX Human PRO1550 cDNA.
DE
XX Human; PRO protein; mapping; se.
XX
XX Homo sapiens.
OS
XX WO200116318-A2.
PN
XX 08-MAR-2001.
PD
XX 24-AUG-2000; 2000MO-US023328.
PF
XX
XX 01-SEP-1999; 99MO-US020111.
PR 15-SEP-1999; 99MO-US021090.
PR 07-DEC-1999; 99US-0169495P.
PR 09-DEC-1999; 99US-0170262P.
PR 11-JAN-2000; 2000US-0175481P.
PR 18-FEB-2000; 2000MO-US004341.
PR 18-FEB-2000; 2000MO-US004342.
PR 22-FEB-2000; 2000MO-US004414.
PR 01-MAR-2000; 2000MO-US005601.
PR 01-MAR-2000; 2000US-0187202P.
PR 21-MAR-2000; 2000US-0191007P.
PR 30-MAR-2000; 2000MO-US008439.
PR 25-APR-2000; 2000US-0199397P.
PR 02-MAY-2000; 2000MO-US014042.
PR 05-JUN-2000; 2000US-0209832P.
XX
XX (GETH) GENENTECH INC.
XX
XX Baton DL, Filvaroff B, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI,

cysoeluglyleghlaaglyleuvalaspvalalailetrpvalglythrlysersp 220

10-SEP-1998 98US-0099763P
10-SEP-1998 98US-0099792P
10-SEP-1998 98US-0099812P
10-SEP-1998 98US-0099812P
10-SEP-1998 98US-0099812P

PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100930P.
PR 22-SEP-1998; 98US-0101279P.
PR 23-SEP-1998; 98US-0101475P.
PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101743P.
PR 24-SEP-1998; 98US-0101916P.
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PR 06-OCT-1998; 98US-0103449P.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021194.
PR 22-DEC-1999; 99WO-US030720.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 01-MAR-2000; 2000WO-US005601.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032378.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.

(GETH) GENENTECH INC.
Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
Grimaldi JC, Gurney AL, Matanabe CK, Wood WI;
P-PSDB; ABG95911.
WPI: 2002-731348/79.

New isolated secreted and transmembrane PRO polypeptide useful for modulating biological activity of a cell, or for treating sports-related joint problems, osteoarthritis or rheumatoid arthritis.

Claim 2, Fig 121, 399pp; English.

The invention relates to an isolated secreted and transmembrane PRO polypeptide having 80 % sequence identity to a sequence appearing as ABG95851-ABG95934 or their associated signal peptide, or a sequence of an extracellular domain of the proteins with their associated signal peptide or lacking its associated signal peptide. Also included are the nucleic acids encoding the proteins, vectors, host cells, fusion proteins and antibodies which specifically bind to the proteins. The proteins are useful for detecting a polypeptide designated as A, B, C or D in a sample suspected of containing an A, B, C or D polypeptide, by contacting the sample with a polypeptide designated as E, F, G, H or I (or vice versa) and determining the formation of a A/E, B/F, B/G, C/H or D/I polypeptide conjugate in the sample, where the formation of the conjugate is indicative of the presence of an A, B, C or D polypeptide in the sample, where A is a PRO10272 polypeptide, B is a PRO20110 polypeptide, C is a PRO10096 polypeptide, D is a PRO19760 polypeptide, E is a PRO5801 polypeptide, F is a PRO1 polypeptide, G is a PRO20060 polypeptide, H is a PRO20233 polypeptide and I is a PRO1890 polypeptide. The sample comprises a cell suspected of expressing the A, B, C or D polypeptide. The E, F, G, H or I polypeptide is labeled with a detectable label or is attached to a solid support. The proteins are useful for linking a bioactive molecule to a cell expressing a polypeptide designated as A, B, C or D or E, F, G,

CC H or I. The bioactive molecule is a toxin, a radiolabel or an antibody.
CC The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H,
CC or I, or antibodies against them are useful for modulating a biological
CC activity of a cell expressing a polypeptide designated as A, B, C or D or
CC E, F, G, H, or I. The cell is killed. The proteins are useful for
CC identifying agonists or antagonists, for the preparation of a medicament
CC useful in the treatment of a condition which is responsive to the
CC proteins, as molecular weight markers for protein electrophoresis
CC purposes, and as therapeutic agents for treating sports-related joint
CC problems, nucleic acids encoding the proteins are useful as
CC arthritides. Nucleic acids encoding the proteins are useful as
CC hybridization probes, in chromosome and gene mapping, in the generation
CC of anti-sense RNA and DNA, for the preparation of the proteins, to
CC generate transgenic or knockout animals which are useful in the
CC development and screening of therapeutic reagents, for chromosome
CC identification, and in gene therapy. The antibody is useful as a
CC therapeutic agent, in a diagnostic assay and for affinity purification of
CC the protein from recombinant cell culture natural sources. The present
CC sequence encodes a novel secreted or transmembrane protein of the
CC invention

XX SQ Sequence 1257 BP, 324 A, 264 C, 299 G, 370 T, 0 U, 0 Other;

Alignment Scores:
Pred. No.: 2,55e-104 Length: 1257
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-10-063-734-122 (1-243) X ABS74438 (1-1257)

QY 1 MetatgProGlnGlyProAlaIaIaSerProGlnArgGlyLeuLeuLeuLeu 20
DB 138 ATGCACCCACGAGGCGCCGCCCTCCCGCAGCGGCTCCGCGCTCTGCTGCTCTG 197
QY 21 LeuLeuGlnLeuProAlaIaIaSerSerAlaSerGlnIleProGlyGlyLeuAla 40
DB 198 CTGCTGAGCTCTCCGCGCGCTGAGCGCTCTGAGATCCCAAGGGAAGCAAGAGCG 257
QY 41 GlnLeuArgGlnArgGlyValValAlaSerLeuIleArgGlyMetCysLeuGlnGlyProAla 60
DB 258 CAGCTCCGCGCAGAGGAGGTGTCGACCTGTATATGCAATGCTTCAAGGCGCAGCA 317
QY 61 GlyValProGlyArgAspGlySerProGlyAlaSerValIleProGlyThrProGlyIle 80
DB 318 GGAGTGTCTGTCGAGACGCGAGCCCTGGGCGCAATGTATTCGGGTACACCTGGGATC 377
QY 81 ProGlyArgAspGlyPheLeuGlyGlyValGlyValGlyValGlyValGlyValGlyVal 100
DB 378 CCAAGTCCGAGATGATTCMAAGAGAGAAAGGAGAAATGCTAGAGAAAGCTTTGAGAG 437
QY 101 SerTTPThProAsnTyrIleGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 120
DB 438 TCTTGACACCCCACTACAGACAGTGTTCATGAGATTCATTAATTAATGATGATCTT 497
QY 121 GlyValIleAlaGlnCysThrPheThrIleMetArgSerAsnSerAlaLeuArgValLeu 140
DB 498 GGAAGAAATTCGAGAGTCAATTTACAAAGAGCGTTCAAAATGATGCTTCAAGAGTTGG 557
QY 141 PheSerGlySerLeuArgLeuIleCysArgAlaAlaCysCysGlnArgTrpTrpPheThr 160
DB 558 TTCAGTGGCTCACTTCGCTTAAATGCAAAATGATGCTGTCAGCGTGTGATTTTCA 617
QY 161 PheAsnGlyAlaGlnCysSerGlyProLeuProIleGlnAlaIleIleIleIleIleIle 180
DB 618 TTCATGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 677
QY 181 GlySerProGlnMetAsnSerThrIleAsnIleIleArgThrSerSerValGlnGlyLeu 200
DB 678 GGAAGCCCTGAATGATCAATTAATTAATTCATTCGACCTTCTGTCGAGAGACTT 737


```

Db      558 TTCAGTGGCTCACTTGGCTAAATGACAAATGACATGCTGACGGTGGATTTCACA 617
Qy      161 PheAenGIyAlaGIuCySeSerGIyProLeuProIIeGIuAlaIleIeTyreLeuAaPgiN 180
Db      618 TTCATGAGAGCTGAATGTTCAAGACCTCTCCATTTGAAGCTATTAATTTATTTGGACCAA 677
Qy      181 GlycerProGIuMeCaAnSerThriLeaenIIehIaArgThSeSerSeValGIuGIyLeu 200
Db      678 GGAAGCCCTGAATGAATTCACATTAATTCATCGACCTCTCTGTGGAAAGACATT 737
Qy      201 CySGluGIyIIeGIyAlaGIyLeuValAaPValaIleIeTyPValGIyThrCySeSerAaP 220
Db      738 TGTGAAGGAATGGTCTGCTGATTAAGTGAATGTTGCTATCTGCGGTGGCACTTGTCAAGAT 797
Qy      221 TyrProLyGIyAaPValaSerThrGIyTrpAaSerValSeSerArgIleIleIeGIuGIu 240
Db      798 TACCCAAAGAGAGATCTTCTACTGATGATGAAATTCAGTTCTGCAATCATTAATTAAGAA 857
Qy      241 LeuProLyS 243
Db      858 CTACCAAAA 866

RESULT 22
AAD32717
ID      AAD32717 standard; cDNA; 1257 BP.
XX
AC      AAD32717;
XX
DT      01-JUL-2002 (first entry)
XX
DE      Human tumour-associated antigenic target-170 (TAT170) cDNA.
XX
KW      Human; tumour-associated antigenic target-170; TAT170; cyrostatic;
KW      gene therapy; tumour; breast; lung; liver; stomach; cancer; ADEPT;
KW      antibody-dependent enzyme mediated prodnug therapy; gene; ss.
XX
OS      Homo sapiens.
XX
FH      Key Location/Qualifiers
FT      CDS 138..866
FT      /tag= a
FT      /product= "Human TAT170 protein"
FT      sig_peptide 138..227
FT      /tag= b
FT      mat_peptide 228..866
FT      /tag= c
FT      /product= "Mature TAT170 protein"
XX
PN      WO200216602-A2.
XX
PD      28-FEB-2002.
XX
PF      23-AUG-2001; 2001MO-US026626.
XX
PR      24-AUG-2000; 2000MO-US023328.
PR      01-DEC-2000; 2000MO-US03678.
PR      28-FEB-2001; 2001MO-US006520.
PR      01-JUN-2001; 2001MO-US017800.
PR      20-JUN-2001; 2001MO-US019692.
PR      29-JUN-2001; 2001MO-US021066.
PR      09-JUL-2001; 2001MO-US021735.
XX
PA      (GETH ) GENENTECH INC.
XX
PI      Ashkenazi AJ, Goddard A, Godowski PJ, Gurney AL, Polakis P,
PI      Williams PM, Wood WI, Wu TD, Zhang Z;
XX
XX      WPI; 2002-292065/33.
XX      P-PSDB; AAE20462.
XX
PT      New antibodies that bind tumor-associated antigenic target (TAT)
PT      polypeptides, useful for treating and diagnosing tumor (e.g. breast,

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PT      lung, liver or stomach tumor) in mammals, e.g. dogs, cats, cattle, pigs,
PT      goats, rabbits or humans.
XX
PS      Claim 1; Fig 2; 124pp; English.
XX
CC      The present invention relates to an isolated antibody that binds to tumor
CC      -associated antigenic target (TAT) polypeptide. The antibody is used for
CC      treating and diagnosing tumors (e.g. breast, lung, liver or stomach
CC      tumors) in mammals, e.g. dogs, cats, cattle, horses, sheep, pigs, goats,
CC      rabbits, or preferably humans. The antibody may also be used in antibody-
CC      dependent enzyme mediated prodnug therapy (ADEPT). The antibody is also
CC      useful for the therapeutic treatment or for the diagnostic detection of
CC      cancer. TAT cDNA is useful in gene therapy. The present sequence is human
CC      TAT170 cDNA designated DNA76393-1664
XX
SQ      Sequence 1257 BP; 324 A; 264 C; 299 G; 370 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,55e-104 Length: 1257
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-10-063-734-122 (1-243) x AAD32717 (1-1257)
Qy      1 MethArgProGIuGIyProAlaAaSerProGIuAaGIuGIyLeuLeuLeuLeu 20
Db      138 ATGCGACCCCGAGGGCCCGCCCTCCCGACGGCGCTCCGCGCTCTGCTGCTCCG 197
Qy      21 LeuLeuGIuLeuProAlaProSeSerAaSerGIuIIeProLyGIyLyGIuLyAa 40
Db      198 CTGCTGACCTGCGCGCGCGCTCGAGCGCTCTGAGATCCCAAGGCGAAGCAAAAGGCG 257
Qy      41 GIuLeuArgGIuArgGIuValAaPLeuTyAaGIyMeCySeLeuGIuGIyProAla 60
Db      258 CAGCTCCGCGACAGGAGGTGTGTGACCTGTATATGAAATGTGTCTACAGGCGCAGCA 317
Qy      61 GIyValProGIyAaArgAaPGLySeProGIyAlaAaValIIeProGIyThrProGIyIIe 80
Db      318 GGAAGTCCCTGCTCGAGACCGGAGCCCTGGGCGCAATGTATATCCCGGTACACCTGGATC 377
Qy      81 ProGIyAaArgAaPGLyPheLyGIyGIuLyGIyGIuCySeLeuArgGIuSePheGIuGIu 100
Db      378 CAAAGTCGAGATGATTCAGAGCAAGAAAGGGGGAATGCTGAGGAAAGCTTTGAGGAG 437
Qy      101 SerTrpThrProAaNTyLyGIyGIuCySeSerTrpSeSerLeuAaNTyGIyIIeAaPLeu 120
Db      438 TCCTGGACACCAACATCAAGCAGTGTTCATGAGTTCATTGAATTATGCAATGATCTT 497
Qy      121 GIyLyIIeAlaGIuCyThrPheThrLyMeCaArgSerAaSerAlaLeuArgValLeu 140
Db      498 GCGAAATATGCGAGGTGATCATTTACAAAGAGCCGTTCAATATAGTCTCTAAGAGTTTG 557
Qy      141 PheSerGIySeLeuArgLeuLyCySeArgAaAaAaCySeGIuAaArgTrpTrpPheTr 160
Db      558 TTCAGTGGCTCACTTGGCTAAATGACAAATGACATGCTGACGGTGGATTTCACA 617
Qy      161 PheAenGIyAlaGIuCySeSerGIyProLeuProIIeGIuAlaIleIeTyreLeuAaPgiN 180
Db      618 TTCATGAGAGCTGAATGTTCAAGACCTCTCCATTTGAAGCTATTAATTTATTTGGACCAA 677
Qy      181 GlycerProGIuMeCaAnSerThriLeaenIIehIaArgThSeSerSeValGIuGIyLeu 200
Db      678 GGAAGCCCTGAATGAATTCACATTAATTCATCGACCTCTCTGTGGAAAGACATT 737
Qy      201 CySGluGIyIIeGIyAlaGIyLeuValAaPValaIleIeTyPValGIyThrCySeSerAaP 220
Db      738 TGTGAAGGAATGGTCTGCTGATTAAGTGAATGTTGCTATCTGCGGTGGCACTTGTCAAGAT 797
Qy      221 TyrProLyGIyAaPValaSerThrGIyTrpAaSerValSeSerArgIleIleIeGIuGIu 240

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Db 798 TACCAAGAGATCTTCTACTGATGATTCATTCGATCATTTATGAGAA 857
 QY 241 LeuProlys 243
 Db 858 CTACCAAAA 866

RESULT 23

ABL95683
 ID ABL95683 standard; cDNA; 1257 BP.

AC ABL95683;
 DT 19-JUL-2002 (first entry)

DE Human angiogenesis related cDNA PRO1550 SEQ ID NO: 245.

KW Human; angiogenesis; PRO protein; cardiovascularization; wound; cancer;
 KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
 KW cardiact; cytosatic; antiangiogenic; hypotensive; vulnerary;
 KW antiarteriosclerotic; gene; ss.

OS Homo sapiens.

PN WO200208284-A2.

PD 31-JAN-2002.

PF 09-JUL-2001; 2001WO-US021735.

PR 20-JUL-2000; 2000US-0219556P.

PR 25-JUL-2000; 2000US-0220624P.

PR 28-JUL-2000; 2000US-0220646P.

PR 02-AUG-2000; 2000US-0222695P.

PR 17-AUG-2000; 2000US-0224365P.

PR 23-AUG-2000; 2000WO-US023522.

PR 24-AUG-2000; 2000WO-US023328.

PR 07-SEP-2000; 2000US-0230978P.

PR 18-SEP-2000; 2000US-00664610.

PR 18-SEP-2000; 2000US-00665350.

PR 24-OCT-2000; 2000US-0242922P.

PR 08-NOV-2000; 2000US-00703238.

PR 08-NOV-2000; 2000WO-US030952.

PR 10-NOV-2000; 2000WO-US030873.

PR 01-DEC-2000; 2000WO-US032678.

PR 20-DEC-2000; 2000US-00747259.

PR 22-JAN-2001; 2001US-00767608.

PR 28-FEB-2001; 2001US-00796498.

PR 01-MAR-2001; 2001WO-US006520.

PR 09-MAR-2001; 2001US-00802706.

PR 14-MAR-2001; 2001US-00808689.

PR 22-MAR-2001; 2001US-00816744.

PR 05-APR-2001; 2001US-00828366.

PR 10-MAY-2001; 2001US-00854208.

PR 25-MAY-2001; 2001US-00860304.

PR 25-MAY-2001; 2001WO-US017092.

PR 30-MAY-2001; 2001US-00870574.

PR 01-JUN-2001; 2001WO-US017800.

PR 20-JUN-2001; 2001WO-US019692.

PA (HILL/) HILLAN K J.
 PA (MARS/) MARSTERS S A.
 PA (PANU/) PAN J.
 PA (PAON/) PAONI N F.
 PA (STEP/) STEPHAN J F.
 PA (WATA/) WATANABE C K.
 PA (WILL/) WILLIAMS P W.
 PA (WOOD/) WOOD W I.

PI Baker KP, Ferrara N, Gerber H, Gertlisen ME, Goddard A,
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF,
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
 DR WPI; 2002-171999/22.
 DR P-PSDB; ABB95545.

PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 PT infarction), endothelial or angiogenic disorders in a mammal.

PS Claim 1, Fig 245; 567pp; English.

CC The present invention provides the protein and coding sequences of human
 CC PRO proteins. These are useful for treating or diagnosing a
 CC cardiovascular, endothelial or angiogenic disorder, including cardiac
 CC hypertrophy, trauma, cancer, age-related macular degeneration,
 CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
 CC healing. The present sequence is a coding sequence of the invention
 CC SQ

Sequence 1257 BP; 324 A; 264 C; 299 G; 370 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2.55e-104 Length: 1257
 Score: 1301.00 Matches: 243
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-10-063-734-122 (1-243) x ABL95683 (1-1257)

QY 1 MetArgProGlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeuLeu 20
 Db 138 ATGGGACCCCAAGGAGCCCGCCGCTCCCGACGCGCTCCGCGGCTCTGCTCTG 197
 QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluLeuProGlyGlyLeuAla 40
 Db 198 CTGCTGAGCTGCGCCGCGCTCGAGCCGCTCGAGATCCCAAGGGGAAACCAAGGCG 257
 QY 41 GlnLeuArgGlnArgGluValValAspLeuTyrAsnGlyMetCysLeuGlnGlyProAla 60
 Db 258 CAGCTCGGAGAGGAGAGCTGTGACCTGTAATGAAATGCTTCAAGGGGCGACGA 317
 QY 61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyTyrProGlyIle 80
 Db 318 GGAGTCCCTGTGCGACCGGAGCCCTGGGCGCAATGTTATCCGGGTAACCTGGGATC 377
 QY 81 ProGlyArgAspGlyPheLeuGlyGluValGlyGlyGlyGlyGlyGlyGlyGlyGly 100
 Db 378 CCAAGTCGGATGATTCACAAAGAGAAAGAGGAGAAATGTCGAGGAAACCTTGAAGAG 437
 QY 101 SerTyrThrProAsnTyrLeuGlnCysSerTyrSerSerLeuAsnTyrGlyIleAspLeu 120
 Db 438 TCCTGACACACCACTACAGAGAGTTCATGAGGATTCATTGAAATTAAGCATAGATCTT 497
 QY 121 GlyValIleAlaGluCysThrPheThrTyrSerThrSerSerAlaLeuArgValLeu 140
 Db 498 GGAATAATTCGGAAGTACATTTACAAAGATGGTCAATATGCTCTTAAGAGTTTGG 557
 QY 141 PheSerGlySerLeuArgLeuLeuCysArgAsnAlaCysCysGlnGlyGlyTyrPheThr 160

Db 558 TTCAGTGGCTCACTTGGCTTAAATGAGAAATGATGCTGTGACGCTTGATTTTACA 617
Qy 161 PheASnglYAlaGluCysSerGlyProLeuProIleGluAlaIleIleTyrLeuAapGln 180
Db 618 TTCATAGAGACTTAATGTTTACAGACCTTCCATTCGATGACCTTAATTTATTTGACCAA 677
Qy 181 GlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGluGlyLeu 200
Db 678 GGAAGCCCTGAATGATTCACACATTAAATTCATTCGACCTTCTCTGTGAGAGACTT 737
Qy 201 CysGluGlyIleGlyAlaGlyLeuValAspValAlaIleTyrValGlyThrCysSerAsp 220
Db 738 TGTGAAGGATTCGTCTGCTGATTAAGTGATGTTGCTATCTGGCTTGCACCTTTCAGAT 797
Qy 221 TyrProIleGlyAspAlaSerThrGlyTyrAsnSerValSerArgIleIleIleGluGln 240
Db 798 TACCCAAAGAGATGCTTCTACTGATGAGATGATTCAGTTTCTGCAATTCATTATTAAGAA 857
Qy 241 LeuProIle 243
Db 858 CTACCAAAA 866
RESULT 24
ID ACA89557 standard; cDNA; 1257 BP.
XX ACA89557;
AC ACA89557;
XX 10-JUL-2003 (first entry)
DT
XX
XX cDNA encoding human PRO polypeptide #183.
DE
XX
XX Human: PRO polypeptide; secreted protein; transmembrane protein;
KM chromosome mapping; gene mapping; tumour; adrenal; lung; colon; breast;
KM prostate; rectal; cervical; liver; cancer; TNF-alpha;
KM tumour necrosis factor-alpha; proliferation; differentiation;
KM chondrocyte cell; bone disorder; cartilage disorder; sports injury;
KM arthritis; cytoskeletal; antiarthritic; osteopathic; gene therapy; gene;
KM 88.
XX
OS Homo sapiens.
XX
PN US2003036141-A1.
XX
PD 20-FEB-2003.
XX
PF 01-JUL-2002; 2002US-00187597.
XX
XX 18-SEP-1997; 97US-0059263P.
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PR 26-AUG-1998; 98US-0097974P.
PR 01-SEP-1998; 98US-0098014P.
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PR 09-SEP-1998; 98US-0099602P.
PR 10-SEP-1998; 98US-0099741P.
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PR 10-SEP-1998; 98US-0099763P.
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PR 25-SEP-1998; 98US-0101786P.
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PR 25-SEP-1998; 98US-0102240P.
PR 29-SEP-1998; 98US-0102330P.
PR 29-SEP-1998; 98US-0102331P.

PR 30-SEP-1998; 98US-0102487P.
PR 30-SEP-1998; 98US-0102570P.
PR 30-SEP-1998; 98US-0102571P.
PR 01-OCT-1998; 98US-0102684P.
PR 01-OCT-1998; 98US-0102687P.

Alignment Scores:

Pred. No. 2,55e-104 Length: 1257
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-10-063-734-122 (1-243) x ACA89557 (1-1257)

QY 1 MetArgProGlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeu 20
DB 138 ATGCGACCCGAGGGGCGCGCGCTCCCGCGAGGCTCCGCGGCTCTGCTGCTG 197
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluLeuProGlyGlyGlnAla 40
DB 198 CTGCTGCGAGCTGCGCGCGCTCCAGCGCTCTGAGATCCCAAGGGAAGAAAGCG 257
QY 41 GlnLeuArgGlnArgGlnValAlaSerLeuThrAlaGlnGlyMetCysLeuGlnGlyProAla 60
DB 258 CAGCTCCGCGAGAGGAGAGTGTGACCTGTATGATGAAATGCTTACAGGCGCAGCA 317
QY 61 GlnValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
DB 318 GAGTGGCTGTGTCAGACGAGGAGCGCTGGGCGCAATGTTATTCGGGTACCTGGAT 377
QY 81 ProGlyArgAspGlyPheLeuGlyGlyGlyGlyGlyCysLeuArgGlnSerPheGlnGlu 100
DB 378 CAGGTGGAGTGTATTAAGAGAAAGAGGGAATGCTGAGGGAAGCTTGAAGAG 437
QY 101 SerThrProAsnThrGlnCysSerThrSerSerLeuAsnThrGlyIleLeuLeu 120
DB 438 TCTGAGACACCACTACAGAGTGTTCATGAGTTCATTGATTAATGCAATGATCTT 497
QY 121 GlnValIleAlaGlnCysThrPheThrLeuMetArgSerAsnSerAlaLeuArgValLeu 140
DB 498 GGGAAATTCGGAGGTGTATTAACAAAGATCCGTTCAATAGTCTTAAGATTTTG 557
QY 141 PheSerGlySerLeuArgLeuLysCysArgAsnAlaCysCysGlnArgThrPheThr 160
DB 558 TTCAGTGGCTCACTTGGCTTAATCAAGAAATGCTGTACAGCTTGTGATTTTCA 617
QY 161 PheAsnGlnAlaGlnCysSerGlyProLeuProIleGlnAlaIleIleTyrlLeuAspGln 180
DB 618 TTCATGAGAGCTGAATGTTCAAGACCTTCCCATTTGAAGCTATATTTTGGACCA 677
QY 181 GlySerProGlnLeuThrAsnSerThrIleAsnIleHisArgThrSerSerValGlnGlyLeu 200
DB 678 GGAAGCCCTGAATGATTCACAAATTAATTAATTCACACTTCTTGTGGAAGACTT 737
QY 201 CysGlnGlyIleGlyAlaGlyLeuValAspValAlaIleIleThrPvalGlyThrCysSerAsp 220
DB 738 TGTGAAGGAATGCTGCTGATTAAGTGAATGCTGATTCATGCTGCTGCTGCTGCTG 797
QY 221 TyrProGlyGlyAspAlaSerThrGlyThrAsnSerValSerArgIleIleIleGlnGlu 240
DB 798 TACCCAAAAGAGATGCTTCTACTGAGATGAAATTCAGTTTCTCCATCATTAATTAAGAA 857
QY 241 LeuProLys 243
DB 858 CTACCAAAA 866
RESULT 25
ACAT3567
ID ACA73567 standard; cDNA; 1257 BP.
XX ACA73567;
AC

XX 01-JUL-2003 (first entry)
XX Human secreted/transmembrane protein (PRO) CDNA #183.
DE Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;
KW proliferation; differentiation; chondrocyte cells;
KW tumour necrosis factor-alpha; TNF-alpha; blood; gene therapy.
XX Homo sapiens.
XX US2003036146-A1.
PD 20-FEB-2003.
XX 02-JUL-2002; 2002US-00187603.
XX 26-JUN-1998; 98US-00105413.
PR 16-SEP-1998; 98WO-US019330.
PR 07-OCT-1998; 98US-00168978.
PR 07-OCT-1998; 98WO-US021141.
PR 06-NOV-1998; 98US-00187368.
PR 01-DEC-1998; 98WO-US025108.
PR 07-DEC-1998; 98US-00202054.
PR 03-MAR-1999; 99US-00254311.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012522.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380139.
PR 25-AUG-1999; 99WO-00380142.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021090.
PR 18-OCT-1999; 99US-00403297.
PR 12-NOV-1999; 99US-00423844.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028551.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 18-FEB-2000; 2000WO-US003431.
PR 18-FEB-2000; 2000WO-US003432.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 08-NOV-2000; 2000US-00709238.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US005520.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00866028.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.

PR 18-JUL-2001; 2001US-00908827.
PR 30-JUL-2001; 2001US-00918585.
PR 06-AUG-2001; 2001US-00924419.
PR 13-AUG-2001; 2001US-00939406.
PR 16-AUG-2001; 2001US-00931836.
PR 28-AUG-2001; 2001US-00941992.
PR 29-AUG-2001; 2001WO-US027099.
PR 04-SEP-2001; 2001WO-US026374.
PR 15-JAN-2002; 2002US-00052586.
XX (GENT) GENENTECH INC.
XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX WPI, 2003-332034/31.
DR P-PSDB; AB086375.
XX Three hundred and five nucleic acids encoding PRO polypeptides, useful in
PT gene therapy, chromosome identification, tissue typing, and for detecting
PT the presence of tumor in a mammal.
XX Claim 2; Fig 365; 707pp; English.
XX The invention relates to three hundred and five nucleic acids encoding
CC PRO polypeptides (secreted and transmembrane), sequences 80% identical to
CC them, or encoding a PRO polypeptide lacking its associated signal peptide
CC or an extracellular domain of the PRO polypeptide, with or lacking its
CC associated signal peptide. Also included are the encoded PRO proteins,
CC PRO expression vectors, host cells transformed with the vector (used to
CC produce PRO proteins), a chimeric molecule comprising the PRO
CC polypeptide fused to a heterologous amino acid sequence, an anti-PRO
CC antibody, a method for stimulating the release of tumor necrosis factor
CC alpha (TNF-alpha) from human blood (by contacting the blood with PRO1079,
CC PRO827, PRO791, PRO1131, PRO1316, PRO1183, PRO1343, PRO1760, PRO1567 or
CC PRO4333), a method for stimulating the proliferation or differentiation
CC of chondrocyte cells by contacting the cells with a PRO6029 polypeptide,
CC a method for detecting the presence of tumor in a mammal and an
CC oligonucleotide probe derived from any of the nucleotide sequences cited
CC above. The PRO polypeptide or anti-PRO antibody is useful for preparing a
CC medicament for treating a condition that is responsive to the PRO
CC polypeptide or anti-PRO antibody. The PRO nucleotide sequences are useful
CC as hybridisation probes in chromosome and gene mapping, or in generating
CC antisense RNA and DNA. PRO nucleic acids are also useful in preparing PRO
CC polypeptides, in assays to identify other proteins or molecules involved
CC in a binding reaction, to generate transgenic animals or knockout
CC animals, which in turn are useful in the development and screening of
CC therapeutically useful reagents, for chromosome identification, and
CC tissue typing. The PRO polypeptides and nucleic acid molecules are also
CC useful for detecting the presence of a tumour in a mammal, stimulating the
CC proliferation or differentiation of chondrocyte cells, stimulating the
CC release of tumour necrosis factor-alpha from human blood, in gene
CC therapy, or as molecular weight markers for protein electrophoresis
CC purposes. The anti-PRO antibodies may be used in diagnostic assays for
CC PRO, or for the affinity purification of PRO from recombinant cell
CC culture or natural sources. The present sequence is a CDNA encoding a PRO
CC protein
XX
XX Sequence 1257 BP; 324 A; 264 C; 299 G; 370 T; 0 U; 0 Other;
SQ
XX
XX Alignment Scores:
Pred. No.: 2 55e-104 Length: 1257
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0
US-10-063-734-122 (1-243) x ACN73567 (1-1257)
QY 1 MetArgProGInGlyProAlaIaIaSerProGInaIrgLeuArgGlyLeuLeuLeuLeu 20
Db 138 ATGCGACCCCAAGGCGCCCGCTCCCGACGCGGCTCCGCGGCTCTGCTGCTCG 197

QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGlnIleProIlyGlyIlyGlnIlyAla 40
 Db 198 CTGCTGACAGCTGCCCGCGCTCGACGCGCTCTGAGATCCCAAGGGGAAAGCAAAAGCG 257
 QY 41 GlnLeuArgGlnArgGlnIlyValIleAspLeuIlyAsnGlyMetCysLeuGlnIlyProAla 60
 Db 258 CAGCTCCGCGCAGAGAGAGGTGTGAGCCGTGTAATGAAATGTGCTTCAAGGGCAGACA 317
 QY 61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyIlyLe 80
 Db 318 GGAGTGCCTGCTGCTGAGACGGAGCCCTGGGCGCAATGTTATTCGGGTACACCTGGGATC 377
 QY 81 ProGlyArgAspGlyPheIlyGlyGlnIlyGlyCysLeuArgGlnIlySerPheGlnIly 100
 Db 378 CCAGTCCGCGATGATTCAGAAAGAGAAAGGGGAAATCTCGAGGAAAGCTTTGAGGAG 437
 QY 101 SerTPThrProAsnIlyIleGlnCysSerTPSerSerLeuAsnIlyGlyIlyAspLeu 120
 Db 438 TCCTGACACCCCACTACAGCAGTTCATGAGTTCATGAGTTCATGAGTTCATGAGTTCAT 497
 QY 121 GlyIlyIleAlaGlyCysThrPheThrIlyMetArgSerAsnSerAlaLeuArgValLeu 140
 Db 498 GGGAAATTCGCGAGTGTACATTTACAAAGATGCTTCATTAATGCTCTAAGAGTTTG 557
 QY 141 PheSerGlySerLeuArgLeuIlyCysArgAsnAlaCysCysGlnArgIlyPheThr 160
 Db 558 TTCAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 617
 QY 161 PheAsnGlyAlaGlyCysSerGlyProLeuProIleGlnIlyIleIlyIlyIlyIlyIly 180
 Db 618 TTCATGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 677
 QY 181 GlySerProGlnLeuAsnSerThrIleAsnIleHisArgThrSerSerValGlnIlyLeu 200
 Db 678 GGAAGCCCTGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAA 737
 QY 201 CysGlnGlyIlyIleGlyAlaGlyLeuValAspValAlaIleThrValGlyIlyCysSer 220
 Db 738 TGTGAAGGAATGT 797
 QY 221 TyrProIlyGlyAspAlaSerThrGlyIlyPheSerValSerArgIleIleIleGlnIly 240
 Db 798 TACCCCAAAAGAGATCTTCTACTGATGATGATGATGATGATGATGATGATGATGAT 857
 QY 241 LeuProIly 243
 Db 858 CTACCAAAA 866
 RESULT 26
 ACA05882
 ID ACA05882 standard; cDNA; 1257 BP.
 XX
 AC ACA05882;
 DT 29-MAY-2003 (first entry)
 XX
 DE Human secreted/transmembrane protein (PRO) cDNA #183.
 XX
 KW Human; gene; ss; secreted and transmembrane protein; PRO; TNF-alpha;
 KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
 KW tissue typing.
 XX
 OS Homo sapiens.
 XX
 FN US2003036162-A1.
 XX
 PD 20-FEB-2003.
 XX
 PF 12-JUL-2002; 2002US-00194423.
 XX
 PR 26-JUN-1998; 98US-00105413.
 PR 16-SEP-1998; 98WO-US019330.
 PT

PR 07-OCT-1998; 98US-00168978.
 PR 07-OCT-1998; 98WO-US021141.
 PR 06-NOV-1998; 98US-00187368.
 PR 01-DEC-1998; 98WO-US025108.
 PR 07-DEC-1998; 98US-00202054.
 PR 03-MAR-1999; 99US-00254311.
 PR 08-MAR-1999; 99WO-US005028.
 PR 14-MAY-1999; 99US-00311832.
 PR 14-MAY-1999; 99WO-US010733.
 PR 02-JUN-1999; 99WO-US012252.
 PR 25-AUG-1999; 99US-00380137.
 PR 25-AUG-1999; 99US-00380138.
 PR 25-AUG-1999; 99US-00380139.
 PR 01-SEP-1999; 99US-00380142.
 PR 15-SEP-1999; 99WO-US020111.
 PR 15-SEP-1999; 99WO-US021090.
 PR 18-OCT-1999; 99US-00403297.
 PR 01-DEC-1999; 99US-00423844.
 PR 01-DEC-1999; 99WO-US028301.
 PR 02-DEC-1999; 99WO-US028551.
 PR 30-DEC-1999; 99WO-US031274.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004432.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 22-AUG-2000; 2000US-00644848.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 18-SEP-2000; 2000US-00664610.
 PR 18-SEP-2000; 2000US-00665350.
 PR 08-NOV-2000; 2000US-00709238.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 22-MAR-2001; 2001US-00815744.
 PR 10-MAY-2001; 2001US-00854208.
 PR 10-MAY-2001; 2001US-00854280.
 PR 25-MAY-2001; 2001US-00866028.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 05-JUN-2001; 2001US-00874503.
 PR 20-JUN-2001; 2001WO-US019699.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 18-JUL-2001; 2001US-00908827.
 PR 30-JUL-2001; 2001US-00918585.
 PR 06-AUG-2001; 2001US-00924419.
 PR 13-AUG-2001; 2001US-00929404.
 PR 16-AUG-2001; 2001US-00931836.
 PR 28-AUG-2001; 2001US-00941939.
 PR 29-AUG-2001; 2001WO-US027099.
 PR 04-SEP-2001; 2001US-00946374.
 PR 15-JAN-2002; 2002US-00052586.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Chen J, Desnoyers L, Goddard A, Goddard PJ, Gurney AL;
 PI Pan J, Smith V, Watanabe CK, Wood WJ, Zhang Z;
 XX
 DR WPI; 2003-332039/31.
 DR P-Psdb; AB067588.
 XX
 PT New secreted and transmembrane PRO polypeptides and nucleic acids, useful

PT in gene therapy, in chromosome and gene mapping, as chromosome markers,
PT in tissue typing, and in chromosome identification.

PS Claim 2; Fig 365; 706pp; English.

XX The invention discloses human nucleic acids encoding secreted and
CC transmembrane (PRO) polypeptides. Also disclosed is an antibody that
CC specifically binds to the PRO polypeptide, a method for stimulating the
CC release of tumour necrosis factor alpha (TNF-alpha) from human blood by
CC contacting the blood with a PRO polypeptide, a method for stimulating the
CC proliferation or differentiation of chondrocyte cells by contacting the
CC cells with a PRO polypeptide, a method for detecting the presence of a
CC tumour in a mammal and an oligonucleotide probe derived from any of the
CC PRO nucleotide sequences. The nucleotide sequences are useful as probes,
CC in chromosome and gene mapping, in generating antisense RNA and DNA, in
CC preparing PRO polypeptides by recombinant techniques and in gene therapy
CC (e.g. for replacement of defective gene). The PRO polypeptides are useful
CC as molecular weight markers for protein electrophoresis purposes, for
CC chromosome identification, as chromosome markers, as therapeutic agents,
CC for stimulating the release of TNF-alpha from human blood, for
CC stimulating the proliferation or differentiation of chondrocytes and
CC detecting the presence of a tumour. The PRO polypeptides and nucleic
CC acids may also be used diagnostically for tissue typing. The sequences
CC presented in ACA05700-ACA06004 are the cDNAs encoding the PRO
CC polypeptides of the invention

XX Sequence 1257 BP; 324 A; 264 C; 299 G; 370 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2,55e-104	Length:	1257
Score:	1301.00	Matches:	243
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	8	Gaps:	0

US-10-063-734-122 (1-243) x ACA05882 (1-1257)

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QY 1 MetATGProGInGlyProAlaAlaSerProGInARgLeuARgLyLeuLeuLeuLeu 20
DB 138 ATGCGACCCCGAGGGCCCCCGCTCCCGACGGCTCCGCGCTCCGCTGCTCCTG 197
QY 21 LeuLeuGInLeuProAlaProSerSerAlaSerGInLeuProAlaGlyLeuAla 40
DB 198 CTGCTCAGCTGCCCCCGCGCTGAGGCTCTGAGATCCCAAGGGAGCAAGAGGCG 257
QY 41 GInLeuARgGInARgGInuValaAlaPLeuTyARngLyMeCyLeuGInGlyProAla 60
DB 258 CAGCTCCGGGAGAGGGAGGTGGTGAACCTGTATATGAAATGTCTTACAAGGGCCAGCA 317
QY 61 GlyValPProGInARgARgLySerProGInAlaAsnValleProGInThPProGIn 80
DB 318 GAGATCCTGCTGAGACCGGAGACCTCGGGCCAAATGTTATTCGGGTACACCTGGGATC 377
QY 81 ProGInARgARgLyPheLySgLyGInuValaGInCyLeuARgGInuSerPheGInu 100
DB 378 CCAAGTCCGGATGATTCANAGAGAAAGGGGAATGTTGAGGAACTTTGAGAGAC 437
QY 101 SerTrpThProAlaNTyLySgInCySerTrpSerSerLeuAlaNTyGlyleAsPLeu 120
DB 438 TCTTGACACCCCACTACAAGCAGTGTTCATGAGTTCAATTGATTAATGCAATGCTT 497
QY 121 GlyLyAlleAlaGInuCyThrPheThrLySMeARgSerARgSerAlaLeuAlaGValleu 140
DB 498 GGGAAATATGGAGAGTACATTACAAAGATCGTTCAATAGTGTCTCAAGAGTTTGG 557
QY 141 PheSerGlySerLeuARgLeuLySARgARgAlaCySARgGInuARgTrpTyPheThr 160
DB 558 TTGAGTGGCTCACTTGGCTAAATGCAAGAAATGCTGCTGAGCGTTGTATTTTCA 617
QY 161 PheAsnGlyAlaGInuCySerGlyProLeuProleGInuAlleleTyLeuAsPIn 180
DB 618 TTCAATGAGAGCTGAATGTTTCAAGACCTCTTCCCATGAGCTAATTAATTATTGACCAA 677
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QY 181 GlySerProGInuMeARgSerThrIleAsnIleHISARgThrSerSerValGInuGlyLeu 200
DB 678 GAAAGCCCTGAATGAAATTCACAACTTATTAATTCATCGACCTTCTCTGAGAGACTT 737
QY 201 CySGInuGlyleGlyAlaGlyLeuValaAlaIleTrpValGlyThrCySerAsp 220
DB 738 TGTGAAGAAATGTTGCTGATTAATGATGATGTTGCTATCTGGGTGGCACTGTTCA 797
QY 221 TyPProLyGlyAlaAspAlaSerThrGlyTrpAsnSerValSerArgIleIleleGInu 240
DB 798 TACCCAAAAGAGAGTCTTCTGATGATGAAATTCAGTTTCTCGCATTAATTGAAGA 857
QY 241 LeuProLyS 243
DB 858 CTACCAAAA 866

RESULT 27
ACA6716
ID ACA6716 standard; cDNA; 1257 BP.
XX
XX ACA6716;
AC
XX
XX 23-JUN-2003 (first entry)
DT
XX
XX cDNA encoding human PRO protein #183.
DE
XX
XX Human; tumour; adrenal; lung; colon; breast; prostate; rectal; cervical;
KW liver; PRO; gene therapy; gene; ss.
XX
XX Homo sapiens.
XX
XX US2003036137-A1.
XX
XX 20-FEB-2003.
XX
XX 27-JUN-2002; 2002US-00184640.
XX
XX 26-JUN-1998; 98US-00105413.
PR 16-SEP-1998; 98WO-US019330.
PR 07-OCT-1998; 98US-00168978.
PR 07-OCT-1998; 98WO-US021141.
PR 06-NOV-1998; 98US-00187368.
PR 01-DEC-1998; 98WO-US025108.
PR 07-DEC-1998; 98US-00202054.
PR 03-MAR-1999; 99US-00254311.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380139.
PR 25-AUG-1999; 99US-00380142.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US020190.
PR 18-OCT-1999; 99US-00403297.
PR 12-NOV-1999; 99US-00423844.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028551.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
```


Pt	xx	Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
Pt	xx	Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
Df	xx	WPI; 2003-401702/38.
Df	xx	P-PsDB; ABU90936.
Pt	xx	New antibody useful for identifying PRO polypeptides, for affinity
Pt	xx	purification of PRO polypeptides, and for preparing a medicament for
Pt	xx	diagnosing or treating conditions responsive to the antibody or PRO
Pt	xx	polypeptide.
Ps	xx	Diclosure; Fig 121; 345pp; English.
Cc	xx	The invention describes an antibody that specifically binds to a PRO
Cc	xx	polypeptide having a fully defined amino acid sequence given in the
Cc	xx	specification. The antibody is useful in identifying PRO polypeptides
Cc	xx	useful for various industrial applications, including pharmaceutical,
Cc	xx	diagnostic, biosensors and bioreactors. The antibody is also used for
Cc	xx	affinity purification of PRO polypeptides from recombinant cell culture
Cc	xx	or natural sources. The antibody, PRO polypeptide, or its agonists or
Cc	xx	antagonists, may be used for preparing a medicament for diagnosing or
Cc	xx	treating a condition responsive to the antibody, PRO polypeptide, or its
Cc	xx	agonists or antagonists. This sequence encodes a novel human secreted and
Cc	xx	transmembrane PRO polypeptide
Sx	xx	Sequence 1257 BP; 324 A; 264 C; 299 G; 370 T; 0 U; 0 Other;
Al	xx	Alignment Scores:
Pr	xx	Pred. No.: 2 55e-104 Length: 1257
Sc	xx	Score: 1301.00 Matches: 243
Pe	xx	Percent Similarity: 100.00% Conservative: 0
Be	xx	Best Local Similarity: 100.00% Mismatches: 0
Qm	xx	Query Match: 100.00% Indels: 0
DB:	xx	8 Gaps: 0
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Qy		1 MetatgProGInGlyProlalalaserProGlnarGlyLeuLeuLeuLeu 20
Db		138 ATGGCAGCCCAAGAGGCCCGCCGCTCCCGACAGGCGTCCGGGCGCTCCGTCGTCTCTG 197
Qy		21 LeuleuGlnleuProlalaproSerSeralaserGlunlleProlYbgIlyBgInlYbAla 40
Db		198 CTGCTGCAGACTCGCCCGCGCTCGACCGCTCTGACATCCCACAAAGGGGAAGCAAAGCGC 257
Qy		41 GlnleuAARGlmarGluValValabpleuTYRanglYwecylseuGnInglyProla 60
Db		258 CAGCTTCGGCAGAAGGAGGTGTGTGACCTGTATAATGAATGTGCTTACAAGGGCCAGCA 317
Qy		61 GlyValalProGlyARgAspGlySePrglyAlaasnValilleProGlyThrProGlyIle 80
Db		318 GGAGTGCCCTGGTCTGACAGCGGACCCTGGGGCCAAATTATTTCCGGGTACACTGGGATC 377
Qy		81 ProGlyARgAspGlyPheIlyBglYbGlyGlyLcyLeuAARGluseRphGIngu 100
Db		378 CCAGGTCCGGATGATTAAGAGAAAGGGGGAATGTCTGAGGGAACCTTGAAGAG 437
Qy		101 SerTPThrProasntYrlYsgInCYserTTPserSerleuananryrGlyilleapleu 120
Db		438 TCCTGGACACCCCAACATCAAGCAGTGTTCATGAGATTCAATTAATGACATAGANTCTT 497
Qy		121 GlyLySillealagLucyThrPhetrrilyMeArSerasnSerallaleuaArgVallleu 140
Db		498 GGGAAAATTGGCGAGTGTACATTTACAAAGATCGCTTCAATATGTGCTCTAAGATTITG 557
Qy		141 PheserGlySerleuarGleuYCyARgAsnalAcYceSyGlnarGTrIPYrPheThr 160
Db		558 TTCAGTGCTCATCTTGCTTAAAAATCAGAAATGATGCTGTACAGGCTTGATTTTACA 617
Qy		161 pheasnglyAlagLucySeserglyProleuProllleGlnalleilelyrleueaspGln 180
Db		618 TTCAATGAGCTGAATGTTCAAGACCTCTTCCAATTGAACCTTAATTTATTTGGACCA 677

Qy	181	GlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGluGlyLeu	200
Db	678	GGAGGCCCTGAATGATTCACATTAATATTCATGCGACTTCTTCTGTGGAGGACTT	737
Qy	201	CysGluGlyIleGlyValAsGlyLeuValAspValAlaIleTyrValGlyThrCysSerAsp	220
Db	738	TGTGAAGGAATTTGGTCTGGATTACTGGATGTCTGCTACTGGCTTGGCACTTGTTAGAT	797
Qy	221	TyrProLyGlyAspAlaSerThrGlyTyrPheSerValSerArgIleIleIleGluGlu	240
Db	798	TACCCAAAAGAGATGCTTCTTCTGATGGAATTCAGTTCTCCGATCATTAATTGAAGAA	857
Qy	241	LeuProLyS 243	
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RESULT 29			
ID	ACD81601	standard; cDNA; 1257 BP.	
AC	ACD81601;		
XX			
DT	18-SEP-2003	(first entry)	
XX			
DE	Human cDNA encoding secreted/transmembrane protein PRO1550.		
KW	Human; ss; gene; secreted/transmembrane protein; PRO; tumour; cancer;		
KW	cytostatic.		
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OS	Homo sapiens.		
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EN	US2003009013-A1.		
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PD	09-JAN-2003.		
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PF	01-MAY-2002;	2002US-00063519.	
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PR	30-DEC-1998;	98KR-00063142.	
PR	08-MAR-1999;	99MO-US005028.	
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PR	02-MAR-2000;	2000MO-US005841.	
PR	21-MAR-2000;	2000MO-US007533.	
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PR	30-MAY-2001;	2001US-00870578.	
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18-JUN-2001; 2001US-00908827.
PR 06-DEC-2001; 2001US-00006867.
XX
PA (GERTH) GENENTECH INC.
XX

PI Eaton DL, Fliviaroff E, Gerritsen ME, Goddard A, Godowski PJ,
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX WPI; 2003-447384/42.
DR P-PSDB; ABO33995.
XX

PT New isolated antibody specifically binding a PRO polypeptide, useful for
PT the preparation of a medicament for treating disorders with the aberrant
PT expression or activity of the PRO polypeptide, such as tumor conditions
PT and cancer.

PS Disclosure; Fig 121; 223pp; English.

XX The invention relates to an antibody that binds to a secreted or
XX transmembrane protein designated PRO1446 appearing as ABO33941. The
XX protein is one of 84 PRO polypeptides which (along with their encoding
XX nucleic acids) are disclosed in the specification. The methods and
XX compositions of the present invention are useful for the preparation of a
XX medicament for the treatment of disorders associated with the aberrant
XX expression or activity of the PRO polypeptide, such as, tumour conditions
XX and cancer. They can also be used to generate transgenic or knockout
XX animals useful in the development and screening of therapeutically useful
XX reagents. The PRO polypeptides and encoding nucleic acids can be used as
XX molecular weight markers for protein electrophoresis, chromosome
XX identification and tissue typing. The antibodies may be used in various
XX diagnostic, competitive binding and/or immunoprecipitation assays. The
XX present sequence encodes a PRO polypeptide

SQ Sequence 1257 BP; 324 A; 264 C; 299 G; 370 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2.55e-104 Length: 1257
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-063-734-122 (1-243) x ACD81601 (1-1257)

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QY 21 LeuLeuGInLeuProAlaProSerSerAlaSerGluIleProGlyGlyLeuAla 40
DB 198 CTGCTGCACTGCGCCGCGCGCTCGAGCCCTCTGAGATCCCAAGGGAAGCAAGGCG 257
QY 41 GInLeuAryGInaGLeuAlaValaIaAspLeuTyraGlyMetCysLeuGInGlyProAla 60
DB 258 CAGCTCCGCGAGGAGGAGTGTGAGCTGTATATGAAATGCTTCAAGGCGCAGCA 317
QY 61 G1YValProG1AryAryG1SerProG1YAlaIaValaIleProG1YThProG1Y1e 80
DB 318 GAGAGGCTGTGTCAGAGAGGAGCCCTGGGCGCAATGTATTCGGGTAACCTGGGATC 377
QY 81 ProG1YArGAspG1YPhelYg1Yg1uYg1YcYsLeuAryG1uSerPhelG1uG1u 100
DB 378 CCAAGTGGGAGTGAATTCAAAGAGAAAGGGGAATGTCTGAAGGAAAGCTTGAAGAG 437
QY 101 SerTrpThrProAsnYrYlYgG1YcYsSerTrpSerSerLeuAlaValaIleAspLeu 120
DB 438 TCCGCAACCACTACAGCACTGTTCATGAGGATTCATTGAAATTTAGCATGATCTT 497
QY 121 G1YlYs11ealag1YsrThrPhelThylYsMetArGserAsnSerAlaLeuAryValleu 140
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QY 141 PheSerGlySerLeuAryLeuAlaCysArGAsnAlaCysCysGlnaGTrpYrPhaThr 160
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QY 161 PheAnGlyAlaGlnCysSerGlyProLeuProIleGlnAlaIleIeYrLeuAspGln 180
DB 618 TTCATGAGACTGAAATGTTCAGAGACTTCTCCATTAAGCTAAATTTATTTGGACCA 677
QY 181 GlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGluGlu 200
DB 678 GGAAGCCCTGAATGAATTCACAACTTAATTTATTCGACTTCTTGAGAGACCTT 737
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DB 738 TGTGAAGAAATGTGGTGTGATGTGATGTGCTATCGGCTGCGACTTGTTCAGAT 797
QY 221 TyrProGlyGlyAspAlaSerThrGlyTrpAsnSerValSerArgIleIleGluGlu 240
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QY 241 LeuProGly 243
DB 858 CTACCCAAA 866
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ID ACP20291
ACFP20291 standard; cDNA; 1257 BP.
ACFP20291;
18-SEP-2003 (first entry)
DE Human secreted polypeptide PRO1550-encoding cDNA, SEQ ID NO:365.
XX
XX KW Human; PRO; secreted protein; transmembrane protein;
KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnery; gene therapy; gene; ss.
XX
XX Homo sapiens.
XX
XX US2003040063-A1.
XX
XX 27-FEB-2003.
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XX 26-JUN-2002; 2002US-00183006.
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Alignment Scores:

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US-10-063-734-122 (1-243) x ACF20291 (1-1257)

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DB 198 CTGCTGAGCTGCCCGCGCCGCTGAGCGCTCTGAGATCCCAAGGGAGCAAAAGGCG 257
QY 41 GlnLeuArgGlnArgGlyValAlaAspLeuTyAsnGlyMetCysLeuGlnGlyProAla 60
DB 258 CAGCTCCGCGAGGAGGTGTGAGCTGTATATGATGATGCTTACAGGCCAGCA 317
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QY 81 ProGlyArgAspGlyPheGlyGlyGlyGlyGlyCysLeuArgGlnSerPheGlnGly 100
DB 378 CCAGGTCCGGATGATTCAAAGAGAAAGGGGAAATGTCTGAGGAAAGCTTTGAGGAG 437
QY 101 SerTrpThrProAsnTyrltyrGlnCysSerTrpSerSerLeuAsnTyrltyrIleAspLeu 120
DB 438 TCTTGAGACCCCACTACAGAGAGTGTTCATGAGATTCATGATTAATGAGTATGATCTT 497
QY 121 GlyIlyAlaGlnCysThrPheThrIlyMetArgSerAsnSerAlaLeuArgValLeu 140
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QY 181 GlySerProGlnMetAsnSerThrIleAsnIleHisArgThrSerSerValGlnGlyLeu 200
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RESULT 31
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ID ACF19677 standard; cDNA; 1257 BP.

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XX AC ACF19677;
XX 17-SEP-2003 (first entry)
DE Human secreted polypeptide PRO1550-encoding cDNA, SEQ ID NO:365.
XX Human; PRO; secreted protein; transmembrane protein;
XX extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
XX chondrocyte; proliferation; differentiation; cartilage disorder;
XX bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
XX adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
XX liver; drug screening; transgenic animal; genetic analysis;
XX antitubercitic; vulnery; gene therapy; gene; ss.
XX Homo sapiens.
XX
XX US2003040064-A1.
XX
XX 27-FEB-2003.
XX
XX 26-JUN-2002; 2002US-00183008.
XX
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KW liver; drug screening; transgenic animal; genetic analysis;
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PR 10-AUG-1998; 98US-0096012P.
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PR 18-SEP-1998; 98US-0101014P.
PR 18-SEP-1998; 98US-0101068P.
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PR 24-SEP-1998; 98US-0101739P.
PR 24-SEP-1998; 98US-0101743P.
PR 24-SEP-1998; 98US-0101922P.
PR 25-SEP-1998; 98US-0101786P.
PR 25-SEP-1998; 98US-0102207P.
PR 29-SEP-1998; 98US-0102240P.
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PR 30-SEP-1998; 98US-0102487P.
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PR 30-SEP-1998; 98US-0102571P.
PR 01-OCT-1998; 98US-0102684P.
PR 01-OCT-1998; 98US-0102687P.

Alignment Scores:
Pred. No.: 2,556-104 Length: 1257
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 8
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DB 138 ATGCACCCCGAGGGCCCGCCGCTCCCGCAGCGGCTCCGCGGCTCCTGCTCCTG 197
QY 21 LeuLeuGInLeuProAlaPserSerAlaSerGInIleProLyGlyLeuGInLyAla 40
DB 198 CTGCTGCAGCTGCCCGCGCTGAGCGCTCTGAGATCCCAAGGAGAAAGAGCGG 257
QY 41 GInLeuArgGInArgGlyValAlaAspLeuTyraGInGlyMetCysLeuGInGlyProAla 60
DB 258 CAGCTCCCGCAGAGGAGGTGTGACCTGTATGCAATGCTTACAGGCGCCAGCA 317
QY 61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
DB 318 GGAGTGCCTGCTCGAGACGGAGCGCTGGGCGCATGTATCCGGGTACCTGGGATC 377
QY 81 ProGlyArgAspGlyPheIleGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100
DB 378 CCAGGTCCGAGTGAATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 437
QY 101 SerTPThrProAsnTyrlsGInCysSerTPSerSerLeuAsnTyrlsIleAspLeu 120
DB 438 TCCTGACACCCCACTACACAGCAGCTTCATGAGATTCATTAATTAATGCAATGATCTT 497
QY 121 GlyIlyIleAlaGlyCysThrPheThrIlyMetArgSerAsnSerAlaLeuArgValLeu 140
DB 498 GGGAAATTCGCGAGGTGATTCATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 557
QY 141 PheSerGlySerLeuArgLeuIleCysArgAsnAlaCysGlyGInArgTPThrPheThr 160
DB 558 TTCAGTGCCTCACTTCGCTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 617
QY 161 PheAsnGlyAlaGlyCysSerGlyProLeuProIleGlyAlaIleIleTyrlsLeuAspGIn 180
DB 618 TTCATGAGCTGAAATGTTCAAGCACTCTCCCATTAAGACTTAATTAATTAATGACCA 677
QY 181 GlySerProGlyMetAsnSerThrIleAsnIleIleIleIleIleIleIleIleIle 200
DB 678 GGAAGCCCTGAAATGATTCACCAATTAATTAATTAATTAATTAATTAATTAATTA 737
QY 201 CysGlyGlyIleGlyAlaGlyLeuValAspValAlaIleTPValGlyThrCysSerAsp 220
DB 738 TGTGAAGGAAATGCTGAGTATGAGATGCTGATCTGAGTGTGCACTTGTGAGAGAT 797
QY 221 TyrProLyGlyAspAlaSerThrGlyTPAsnSerValSerArgIleIleIleGlyGIn 240
DB 798 TACCCAAAGAGAGATTCCTTCACTGAGTGAATTCAGTTTCTCGCATCTTAATGAAGA 857
QY 241 LeuProLyS 243
DB 858 CTACCAAAA 866
RESULT 34
ACD25233
ID ACD25233 standard; cDNA; 1257 BP.
XX
AC ACD25233;
DT 30-AUG-2003 (first entry)
XX
DE Human secreted/transmembrane protein (PRO) cDNA #183.
XX
KW Human; gene; ss; secreted and transmembrane protein; PRO; TNF-alpha;

KM tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
KM tissue typing; adrenal tumour; lung tumour; colon tumour; breast tumour;
KM prostate tumour; rectal tumour; cervical tumour; liver tumour.

OS Homo sapiens.

XX US2003044925-A1.

XX 06-MAR-2003.

XX 25-JUN-2002; 2002US-00180560.

XX 18-SEP-1997; 97US-0059263P.

PR 18-SEP-1997; 97US-0059266P.

PR 17-OCT-1997; 97US-0062250P.

PR 21-OCT-1997; 97US-0063486P.

PR 24-OCT-1997; 97US-0063120P.

PR 24-OCT-1997; 97US-0063121P.

PR 28-OCT-1997; 97US-0063540P.

PR 28-OCT-1997; 97US-0063541P.

PR 28-OCT-1997; 97US-0063544P.

PR 28-OCT-1997; 97US-0063564P.

PR 29-OCT-1997; 97US-0063734P.

PR 31-OCT-1997; 97US-0063870P.

PR 31-OCT-1997; 97US-0064103P.

PR 13-NOV-1997; 97US-0065311P.

PR 21-NOV-1997; 97US-0066120P.

PR 24-NOV-1997; 97US-0066466P.

PR 11-DEC-1997; 97US-0066772P.

PR 11-DEC-1997; 97US-0069335P.

PR 17-DEC-1997; 97US-0069425P.

PR 18-DEC-1997; 97US-0069870P.

PR 10-MAR-1998; 98US-0077450P.

PR 11-MAR-1998; 98US-0077632P.

PR 20-MAR-1998; 98US-0077639P.

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PR 27-MAR-1998; 98US-0078939P.

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PR 09-JUN-1998; 98US-0088217P.

PR 10-JUN-1998; 98US-0088655P.

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PR 17-JUN-1998; 98US-0089538P.

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PR 18-JUN-1998; 98US-0089653P.

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PR 22-JUN-1998; 98US-0090252P.

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PR 25-JUN-1998; 98US-0090688P.

PR 25-JUN-1998; 98US-0090689P.

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PR 26-JUN-1998; 98US-0090862P.

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PR 26-JUN-1998; 98US-0091010P.

PR 01-JUL-1998; 98US-0091359P.

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PR 26-AUG-1998; 98US-0097954P.

PR 26-AUG-1998; 98US-0097955P.

PR 26-AUG-1998; 98US-0097971P.

PR 26-AUG-1998; 98US-0097974P.
PR 26-AUG-1998; 98US-0098014P.
PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098723P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 09-SEP-1998; 98US-0099602P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099754P.
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PR 16-SEP-1998; 98US-0100662P.
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PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100683P.
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PR 06-OCT-1998; 98US-0103449P.

Alignment Scores:

Pred. No.: 2,55e-104 Length: 1257
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

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QY 21 LeuLeuGInLeuProAlaProSerSerAlaSerGInLeuProArgGlyLeuArgAla 40
DB 198 CTGCTCAGCTGCGCCGCGCGCTGAGCGGCTCTGAGATCCCAAGGAGGAAAGGCG 257
QY 41 GInLeuArgGInArgGInuValValaLeuLeuTyraSerGlyMetCysLeuGInGlyProAla 60
DB 258 CAGCTCCGGCAGAGGAGGAGGCTGAGCTGTATTAATGGAATGCTTACAGGCGCAGCA 317
QY 61 GInValProGInArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
DB 318 GGAGTCCCTGCTGAGAGCGGAGCCCTGGGGCCAAATGTTATTCGGGTACACCTGGGATC 377
QY 81 ProGInArgAspGlyPheLeuGlyGInuValGlyGInCysLeuArgGInuSerPheGInuGIn 100

DB 378 CCAGGTCGGAGTGAATTCAAAGAGAAAGGGGAAATGCTGAGGAAAGCTTTGAGGAG 437
QY 101 SerTrpThrProAsnTrpTyrLeuGInCysSerTrpSerSerLeuAsnTrpGlyIleAspLeu 120
DB 438 TCCTGGACACCCCACTACACAGAGTGTTCATGTGAGCTTCATGAAATTAATGCGATTAATCTT 497
QY 121 GInuValIleAlaGInCysThrPheThrTyrMetAcGSerAsnSerAlaLeuArgValLeu 140
DB 498 GGGAAATTCGGAGTGTACATTTCAAGATGCTTCAAATATGTCCTTAAGAGTTTG 557
QY 141 PheSerGlySerLeuArgLeuLysCysArgAsnAlaCysCysGInArgTrpTyrPheThr 160
DB 558 TTCAGTGCTCACTTCGGCTAAATGCAAGAAATGCATGCTGCACGCTTGATTTTCA 617
QY 161 PheAsnGlyAlaGInCysSerGlyProLeuProIleGInuAlaIleIleTyrLeuAspGIn 180
DB 618 TTCAAATGAGCTGAATGTTCAGAGCTCTCCCATTTGAAGCTATTAATTTTGAACCA 677
QY 181 GInSerProGInuMetAsnSerThrIleAsnIleHisArgThrSerSerValGInuGInu 200
DB 678 GGAAGCCTGAATATGATTCACAAATTAATTCATCGCACTTCTTCTGTGAGAGACTT 737
QY 201 CysGInuGlyIleGlyAlaGlyLeuValaLeuValaIleTrpValGlyThrCysSerAsp 220
DB 738 TGTGAAGAAATGCTGCTGCTGATTAATGATGTTCATCTATCTGGCTTGACACTTGCAGAT 797
QY 221 TyrProLysGlyAspAlaSerThrGlyTyrAsnSerValSerArgIleIleIleGInu 240
DB 798 TACCAAAAGAGAGATGCTTCTACTGATGAGATTCAGTTTCGCACTCATTTATGAAGAA 857
QY 241 LeuProLys 243
DB 858 CTACCAAAA 866
RESULT 35
ACF00282
ID ACF00282 standard; cDNA; 1257 BP.
XX AC F00282;
XX 19-SEP-2003 (first entry)
DE Human secreted polypeptide PRO1550-encoding cDNA, SEQ ID NO:365.
XX
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XX Human; PRO; secreted protein; transmembrane protein;
KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnerary; gene therapy; gene; ss.
OS
XX Homo sapiens.
XX
PN US2003054474-A1.
PD 20-MAR-2003.
XX
XX
PF 22-JUL-2002; 2002US-00201530.
XX
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PR 22-JUN-1998; 98US-0090254P.
PR 02-JUN-1999; 99WO-US012252.
PR 25-AUG-1999; 99US-00380137.
PR 28-FEB-2001; 2001WO-US006520.
PR 15-JAN-2002; 2002US-00052586.
XX
XX
PA (GETH) GENENTECH INC.
XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2003-503631/47.

PT a medicament for treating a condition that is responsive to the PRO
PT polypeptide or antibody.

PS Disclosure; Fig 121; 409pp; English.

XX The invention describes novel isolated PRO polypeptides. The PRO
CC polypeptides or anti-PRO antibodies are useful in preparing a medicament
CC for treating a condition that is responsive to the PRO polypeptide or
CC antibody. The PRO nucleotide sequences may be used as hybridisation
CC probes in chromosome and gene mapping, or in generating antisense RNA and
CC DNA. PRO nucleic acids are also useful in preparing PRO polypeptides. In
CC assays to identify other proteins or molecules involved in binding
CC reaction, to generate transgenic animals or knockout animals, which in
CC turn are useful in the development and screening of therapeutically
CC useful reagents, for chromosome identification, and tissue typing. The
CC PRO polypeptides and nucleic acid molecules are also useful in gene
CC therapy, and as molecular weight markers for protein electrophoresis
CC purposes. The anti-PRO antibodies may be used in diagnostic assays for
CC PRO, or for the affinity purification of PRO from recombinant cell
CC culture or natural sources. This sequence encodes a novel human secreted
CC and transmembrane PRO polypeptide

XX Sequence 1257 BP; 324 A; 264 C; 299 G; 370 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2,55e-104	Length:	1257
Score:	1301.00	Matches:	243
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	8	Gaps:	0

US-10-063-734-122 (1-243) x ACA60423 (1-1257)

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QY 1 MetAArgProGlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeuLeu 20
DB 138 ATGCCAGCCACGAGGCCCCCGCGCTCCCGACGGCTCCGCGCTCTGCTGCTCTG 197
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluLeuProGlyGlyGlyGlyGly 40
DB 198 CTGCTGACACTGCTCCCGCGCTGAGCGCTCTGAGATCCCAAGGAGCAAAAGGGCG 257
QY 41 GlnLeuArgGlnArgGlnValValAlaPleuArgGlyGlyGlyGlyGlyGlyGly 60
DB 258 CAGCTCCGCGACAGGAGGAGTGGTGGACCTGTATATGAGATGCTTACAGGCCACGA 317
QY 61 GlyValProGlyArgArgGlySerProGlyAlaAlaValIleProGlyThrProGly 80
DB 318 GAGTGTCTGTGTGAGACGGGAGCCCTGGGGCCAAATGTTATTCGGGTACACTGGATC 377
QY 81 ProGlyArgArgGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100
DB 378 CCAAGTCGGAGTGTGATTAAGAGAAAGGGGAAATGCTGAGGAAAGCTTTGAGAG 437
QY 101 SerTyrThrProAlaTyrIleGlnGlySerTyrSerSerLeuAlaTyrGlyIleAsp 120
DB 438 TCTGTGACACCCACACTACAGACGATTTCAAGATGCGTTCAAAATGCTCTTAAGATT 497
QY 121 GlyValIleAlaGlnGlyThrPheThrIleMetArgSerArgSerAlaLeuArgVal 140
DB 498 GGGAAATATGGGAGTGTACATTTACAAAGATGCTCAAAATGCTCTTAAGATT 557
QY 141 PheSerGlySerLeuArgLeuArgGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 160
DB 558 TTCAGTGGTCTCACTTGGCTAAATGCAAGAAATGCTGAGGCTTGAATTTTCA 617
QY 161 PheArgGlyAlaGlnGlySerGlyProLeuProIleGluAlaIleIleIleIle 180
DB 618 TTCAGTGGTCTCACTTGGCTAAATGCAAGAAATGCTGAGGCTTGAATTTTCA 677
QY 181 GlySerProGlyLeuArgSerThrIleAlaIleIleIleIleIleIleIleIle 200
DB 678 GGAAGCCCTGAAATGAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 737
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QY 201 CysGluGlyIleGlyValAlaGlyLeuValAlaIleTyrValGlyThrCysSerAsp 220
DB 738 TGTGAAAGAAATGAGTGGCTGATTAAGTATGATGCTTCTGATGCTGCTGATGAT 797
QY 221 TyrProGlyGlyAspAlaSerThrGlyTyrPheSerValSerArgIleIleIleGlu 240
DB 798 TACCCAAAAGAGAGTCTTACTGATGAAATTCAGTTTCCGATCATTAATTAAGAA 857
QY 241 LeuProGly 243
DB 858 CTACCAAAA 866
RESULT 37
ACA72339
ID ACA72339 standard; cDNA; 1257 BP.
XX
AC ACA72339;
XX
DT 30-JUN-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO1550 cDNA.
XX
KW Human; secreted and transmembrane protein; PRO; cytosolic; gene therapy;
KW chondrocyte stimulator; chromosome mapping; gene mapping;
KW transgenic animal; knock-out animal; tumour; gene; ss.
XX Homo sapiens.
XX US2003032114-A1.
XX
PD 13-FEB-2003.
XX
PF 20-JUN-2002; 2002US-00176919.
XX
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
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PR 21-OCT-1997; 97US-0063486P.
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Alignment Scores:
Pred. No.: 2,55e-104
Score: 1301.00
Length: 1257
Matches: 243

Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 100.00%
 DB: 8
 Gaps: 0

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 QY 81 ProGlyArgAspGlyPheLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100
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ACD04863
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ACD04863;

ACD04863; 06-AUG-2003 (first entry)

XX 06-AUG-2003 (first entry)

DE Novel human secreted and transmembrane protein PRO1550 cDNA.

KM Human; ss; gene therapy; tumour necrosis factor alpha; TNF-alpha;

KW Chondrocyte stimulation; tumour; tissue typing; gene.

OS Homo sapiens.

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Alignment Scores:

Pred. No.: 2,55e-104
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 Gaps: 0

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 QY 81 ProGlyArgArgGlyPheLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100
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QY 121 GlyValIleAlaGluCysThrPheThrIleMetArgSerAsnSerAlaLeuArgValLeu 140
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QY 141 PheSerGlySerLeuArgLeuArgCysArgAsnAlaCysCysGlnArgTrpPheThr 160
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QY 181 GlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGluGlyLeu 200
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AC ACD18324;
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DT 26-AUG-2003 (first entry)
DE Human secreted/transmembrane protein (PRO) cDNA #183.
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KW Human; gene; ss; secreted and transmembrane protein; PRO; TNF-alpha;
KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
KW tissue typing; adrenal tumour; lung tumour; colon tumour; breast tumour;
KW prostate tumour; rectal tumour; cervical tumour; liver tumour.
XX
OS Homo sapiens.
XX
PN US2003036124-A1.
XX
PD 20-FEB-2003.
XX
PF 26-JUN-2002; 2002US-00180998.
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PR 18-SEP-1997; 97US-0059263P.
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PR 06-OCT-1998; 98US-0103258P.
PR 06-OCT-1998; 98US-0103449P.

Alignment Scores:

Pred. No.: 2,556-104 Length: 1257
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 8

US-10-063-734-122 (1-243) x ACD18324 (1-1257)

QY 1 MetArgProGInGInGProAlaIaSerProGInArgLeuArgGlyLeuLeuLeuLeu 20
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QY 21 LeuLeuGInLeuProAlaIaProSerSerAlaSerGluIleProLyGlyGlyGlyGly 40
Db 198 CTGCTGACAGCTCCCGCCGCTCGAGGCTCTGAGATCCCAAGGAGGAAAGGCG 257
QY 41 GlnLeuArgGlnArgGlnValIaIaPLeuTyraSngIyMeCysLeuGlnGlyProAla 60
Db 258 CAGCTCCGCGAGAGGAGGAGTGAGACCTGTATATGATGATGCTTCAAGGCGACCA 317
QY 61 GlyValProGInArgArgGlySerProGInIaIaSerValIleProGlyThrProGlyIle 80
Db 318 GAGTGCCTGTGTGAGAGCGGAGCCCTGGAGCCCAATGATATCCGGATACCTGGATC 377
QY 81 ProGInArgArgGlyPheLySngIyGlyGlyCysLeuArgGlySerPheGlyGln 100
Db 378 CAGGTGCGATGATTCACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 437
QY 101 SerThrProLeuTyIySngIyCysSerTyrSerSerLeuAsnTyGlyIleAspLeu 120
Db 438 TCCGGACACCCACACACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 497
QY 121 GlyLySleIaIaGluCysThrPheThrLySMeIaGSerAnSerAlaLeuArgValLeu 140
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QY 161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGluIaIleIleTyLeuAspGln 180
Db 618 TTCATGAGAGCTGATGTCAGAGCTCTTCCCATGAAAGTATATTTTGGACCA 677
QY 181 GlySerProGluMeIaSerThrIleAsnIleHisArgThrSerSerValGlnGlyLeu 200
Db 678 GGAAGCCCTGAATGAATTCACATTAATTCATCCACTTTCTTGGAAGACCTT 737
QY 201 CysGlnGlyIleGlyAlaGlyLeuValAspValaIleTyrValGlyThrCysSerAsp 220
Db 738 TGTGAAGGATGGTGGAGTGTAGTGTCTTCTGCGGTGGCACTTCTTCAGAT 797
QY 221 TyrProLySngIyAspAlaSerThrGlyTyrAsnSerValSerArgIleIleGlnGln 240
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QY 241 Leuprolide 243
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Db 858 CTRACAAA 866

RESULT 40
ACD08331
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ACD08331,
ACD08331,
09-AUG-2003 (first entry)

Human secreted/transmembrane protein (PRO) cDNA #183.

Human; gene; ss; secreted and transmembrane protein; PRO; TNF-alpha;
tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
tissue typing; adrenal tumour; lung tumour; colon tumour; breast tumour;
prostate tumour; rectal tumour; cervical tumour; liver tumour.

OS Homo sapiens.
XX
XX US2003040054-A1.
XX
PD 27-FEB-2003.
XX
PF 20-JUN-2002; 2002US-00176479.
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PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
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PR 28-OCT-1997; 97US-0063541P.
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Alignment Scores:

Pred. No.: 2,55e-104 Length: 1257
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-10-063-734-122 (1-243) x ACD08331 (1-1257)

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Db 198 CTCTGCGAGCTCCCGCCCGCTCGAGCCCTCTAGATCCCAAGGGGAAAGCAAGGCC 257
Qy 41 GlnLeuAlaGlnInaRgtGlnAlaValAlaSerLeuTyrAsnGlyGlnCysLeuGInGlyProAla 60
Db 258 CAGCTCCGCGAGGAGGAGGTGGTGGACCTGTATATAGGATGCTTACAGGCCAGCA 317
Qy 61 GlyValProGInYArGAspGlySerProGInYAlaSerValLeuProGInYThrProGInYIle 80
Db 318 GGAGTCCCTGGTCGAGCGGAGCCCTGGGGCCCATGTTTCCGGGTACACCTGGGATC 377
Qy 81 ProGInYArGAspGlyPheLeuGlyGlnGlyGlnGlyGlnGlyGlnGlyGlnGlyGlnGlyGln 100
Db 378 CCAGGTCCGGGATGATTCATTAAGAGAAAGGGGAAATGTTGAGGAAAGCTTGGAGAG 437
Qy 101 SerTPThrProAsnTyrGlnGlnCysSerTyrSerSerLeuAsnTyrGlyIleAspLeu 120
Db 438 TCTGGACACCACTACAGAGCTGTCATGAGTTCATTAATGATTAATGATTAATGATTAATGATTAAT 497
Qy 121 GlyValIleAlaGlnCysThrPheThrLysMetArgSerAsnSerAlaLeuRyValLeu 140
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09-JUL-2003 (first entry)
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KW Human; se; gene therapy; chondrocyte stimulation; TNF-alpha release;
KW chondrocyte proliferation; chondrocyte differentiation; tumour detection;
KW tissue typing; gene.
XX
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XX 20-FEB-2003.
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XX 27-JUN-2002; 2002US-00184630.
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KW chondrocyte stimulator; chromosome mapping; gene mapping;
KW transgenic animal; knockout animal; tissue typing;
KW chondrocyte proliferation; chondrocyte differentiation;
KW tumour necrosis factor-alpha stimulation; TNF-alpha stimulation; gene;
KW ss.
XX
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Alignment Scores:

Pred. No.: 2,556-104
Score: 1301.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
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DB: 8
Gaps: 0

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QY 41 GlnLeuArgGlnArgGluValIaIaIeLeuTYraGlnGlyMetCysLeuGlnGlyProAla 60
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XX ACD15972;
AC ACD15972;
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XX Human: Gene; ss; secreted and transmembrane protein; PRO; TNF-alpha;
KM tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
KM tissue typing; adrenal tumour; lung tumour; colon tumour; breast tumour;
KM prostate tumour; rectal tumour; cervical tumour; liver tumour.
XX Homo sapiens.
OS US2003027324-A1.
XX PN 06-FEB-2003.
XX PD 21-JUN-2002; 2002US-00176991.
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 PR 30-SEP-1998; 98US-0102571P.
 PR 01-OCT-1998; 98US-0102684P.
 PR 01-OCT-1998; 98US-0102687P.
 PR 02-OCT-1998; 98US-0102965P.
 PR 06-OCT-1998; 98US-0103258P.
 PR 06-OCT-1998; 98US-0103449P.

Alignment Scores:
 Pred. No.: 2,556-104 Length: 1257
 Score: 1301.00 Matches: 243
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 8 Gaps: 0

US-10-063-734-122 (1-243) x ACD15972 (1-1257)

QY 1 MetArgProGlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeuLeu 20
 DB 138 ATGCACCCCGAGGCGCCGCCCTCCCGCAGCGGCTCCGCGGCTCCTGCTCCTG 197

QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluLeuProGlyGlyLeuAla 40
 DB 198 CTGCTGCACGCTCCCGCGCGCTGAGCGCTCTGAGATCCCAAGGGAAGAAAGGCG 257

QY 41 GlnLeuArgGlnArgGluValAlaLeuLeuTyraGlnMetCysLeuGlnGlyProAla 60
 DB 258 CAGCTCCCGCAGAGGAGGTGTGACCTGTATATGAAATGCTTACAGAGGCCAGCA 317

QY 61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
 DB 318 GGAAGTGGCTGTGAGAGCGGAGCCCTGGGCGCAATGTATTCCGGTACACTGGAGATC 377

QY 81 ProGlyArgAspGlyPheLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100
 DB 378 CCAGGTCCGAGTGAATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 437

QY 101 SerTyrThrProAsnTyrIleGlnCysSerTyrSerSerLeuAsnTyrGlyIleAspLeu 120
 DB 438 TCTTGACACCCCACTACAGAGAGTGTTCATGAGTTCATTGAATTAATGCAATGATCTT 497

QY 121 GlyIleAlaGluCysThrPheThrIleMetArgSerAsnSerAlaLeuArgValLeu 140
 DB 498 GGAAGAAATTCGAGAGTATCATTTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 557

QY 141 PheSerGlySerLeuArgLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 160
 DB 558 TTCAGTGGCTCACTTCGCTAAATGCAAGATGATGCTGACAGCTGTGATTTTCA 617

QY 161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleTyrLeuAspGln 180
 DB 618 TTCATGAGCTGATGATTTTCAAGAGCTTCCCATTTGAGACTTATTTATTTGAGACCA 677

QY 181 GlySerProGluMetAsnSerThrIleAsnIleIleIleIleIleIleIleIleIleIle 200
 DB 678 GGAAGCCCTGAATGATTTCAACATTTATATTTCACTTCTTGTGAGAGACTT 737

QY 201 CysGluGlyIleGlyAlaGlyLeuValAlaIleIleIleIleIleIleIleIleIleIle 220
 DB 738 TGTGAAGGATGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 797

QY 221 TyrProLeuGlyAspAlaSerThrGlyTyrPasnSerValSerArgIleIleIleGluGln 240
 DB 798 TACCAAAAGAGAGCTTCTTCACTGATGATGATGATGATGATGATGATGATGATGATG 857

QY 241 LeuProIle 243
 DB 858 CTACCAAAA 866

RESULT 46
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 DT 27-AUG-2003 (first entry)
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 KW Human; secreted and transmembrane protein; PRO; chromosome mapping;

PR 16-AUG-2001; 2001US-00931886.
PR 28-AUG-2001; 2001US-00941992.
PR 29-AUG-2001; 2001MO-US027092.
PR 04-SEP-2001; 2001US-00946374.
PR 15-JAN-2002; 2002US-00052586.
PA (GENTH) GENENTECH INC.
PI Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL,
PI Pan U, Smith V, Watanabe CK, Wood WT, Zhang Z,
PI MPI; 2003-402071/38.
DR F-PSDB; ABO19293.
XX
XX
XX New secreted and transmembrane PRO polypeptides and nucleic acids, useful
PT in gene therapy, chromosome identification, tissue typing, for detecting
PT the presence of tumor in a mammal, or as hybridization probes in gene
PT mapping.

XX
XX
XX Claim 2; SEQ ID NO 365; 707pp; English.

CC The invention describes a novel isolated PRO polypeptide. The PRO
CC polypeptide or anti-PRO antibody is useful for preparing a medicament for
CC treating a condition that is responsive to the PRO polypeptide or anti-
CC PRO antibody. The PRO nucleotide sequences are useful as hybridisation
CC probes in chromosome and gene mapping, or in generating antisense RNA and
CC DNA. PRO nucleic acids are also useful in preparing PRO polypeptides, in
CC assays to identify other proteins or molecules involved in binding
CC reaction, to generate transgenic animals or knockout animals, which in
CC turn are useful in the development and screening of therapeutically
CC useful reagents, for chromosome identification, and tissue typing. The
CC PRO polypeptides and nucleic acid molecules are also useful for detecting
CC the presence of tumour in a mammal, stimulating proliferation or
CC differentiation of chondrocyte cells, stimulating the release of tumour
CC necrosis factor-alpha from human blood, in gene therapy, or as molecular
CC weight markers for protein electrophoresis purposes. The anti-PRO
CC antibodies may be used in diagnostic assays for PRO, or for the affinity
CC purification of PRO from recombinant cell culture or natural sources.
CC This sequence encodes a novel human secreted and transmembrane PRO
CC polypeptide

SQ Sequence 1257 BP; 324 A; 264 C; 299 G; 370 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,55e-104 Length: 1257
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-10-063-734-122 (1-243) x ACD25540 (1-1257)

DY 1 MetAyrProglnglYProAlaIAsSerProGlNaArgLeuAarglyLeuLeuLeuLeu 20
Db 138 ATCGACGCCCAAGGGCCCCCGCCTTCCCGCAGCGGCTCCGCGCTCTGCCTCTTG 197
DY 21 LeuLeuGlnLeuProAlaProIAsSerSeRAlAsSerGluIleProlYSgLYsgInLYsAla 40
Db 198 CTGCTCAACTCCCGCGCGCTCGAGCCCTCTGAATCCCACAAAGGGAACAAAAGCG 257
DY 41 GlnLeuAyrGlnAargGlnValValAspLeuTyrsengLywecCySLeuGlnGlyProAla 60
Db 258 CACTTCGGACAAGGAGGTGTGACCTGTATATAGMAATGCTTTACAAGGGCCAGCA 317
DY 61 GlYvalProglYarGASPdlYserProglYlaIsanValIleProglYThrProglYile 80
Db 318 GGAGTGCCTGCTCGAGACGGAGCCCTGGGCGCAATTMTTCGGGTAACTCGGAGTC 377
DY 81 ProGlYarGArngclYPhelYsgLYglULySgLYglucYsLeuArgIusErPhegluGln 100
Db 378 CCAAGTCCGGATGAGTTTCAAAGGAGAAAGGGGGAATGTCTGAGGGAACCTTTGAGGAG 437

QY 101 SerTrpThProAsnTyrIleGlnCysSerTrpSerSerIleuAsnTyrIleAePleu 120
| | | | |
Db 438 TCCTGGACACCCACACACAGAGTTCATGAGTTCATTAATGATGATGATCTT 497
| | | | |
QY 121 GilylVsiIleAlaGlnCysThrPheThrIlyMetArgSerAsnSerAlaIleuArgValIleu 140
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Db 498 GGGAAATGCGAGAGTACATTTACAAAGATCGTTCAAAATGATGCTCTTAAGAGTTTG 557
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QY 141 PheSerGlySerIleuArgIleuIysCysArgAsnAlaCysCysGlnArgTrpPheThr 160
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Db 558 TTCAGAGGCTCAGCTTCGCTAAATGACAAAGATGCTGTCAGGCTTGATTTCAACA 617
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QY 161 PheAsnGlyAlaGlnCysSerGlyProIleuProIleGlnAlaIleIleTyrIleuAeGln 180
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Db 618 TTCATGAGCTGAAATGTTCAAGACCTTCCCATTTGAACTTAATTTTGGACCA 677
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QY 181 GlySerProGlnMetAsnSerThrIleAsnIleIleArgThrSerSerValGlnIleu 200
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Db 678 GGAAGCCCTGAATGATTAATCAACATTAATTCATCGACCTTCTGGAAGGACTT 737
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QY 201 CysGlnGlyIleGlnValIleuValaIlePvalAlaIleTrpValGlyThrCysSerAap 220
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Db 738 TGTGAAGAAATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 797
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QY 221 TyrProIyGlyAspAlaSerThrGlyTrpAsnSerValSerArgIleIleIleGlnIle 240
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Db 798 TACCCAAAGAGATCTTCTACTGATGATGATGATGATGATGATGATGATGATGATGAT 857
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QY 241 LeuProIyS 243
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Db 858 CTACCAAAA 866
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RESULT 47
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ID ACD18017 standard; cDNA; 1257 BP.
AC
XX ACD18017;
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XX 25-AUG-2003 (first entry)
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XX Human; gene; 88; secreted and transmembrane protein; PRO; TNF-alpha;
XX tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
XX tissue typing; adrenal tumour; lung tumour; colon tumour; breast tumour;
XX prostate tumour; rectal tumour; cervical tumour; liver tumour.
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XX Homo sapiens.
XX
XX US2003036123-A1.
XX
XX 20-FEB-2003.
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XX 25-JUN-2002; 2002US-00180551.
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PR 12-DEC-1997; 97US-0069425P.
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Alignment Scores:
 Pred. No.: 2,556-104
 Score: 1301.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 100.00%
 DB: 8
 Gaps: 0

US-10-063-734-122 (1-243) x ACD18017 (1-1257)

QY 1 MetArgProGlnGlyProAlaAlaSerProGlnArgGlyLeuLeuLeuLeu 20
 DB 138 ATGCGACCCCGAGGCGCCCGCGCTCCCGACGGCTCCGCGCTCTGCTCTG 197
 QY 21 LeuLeuGlnLeuProAlaPProSerAlaSerGlyIleProGlyGlyLeuAla 40
 DB CTGCTGCGAGCTCCCGCGCGCTGAGCGCTGAGATCCCAAGGGAAGCAAAAGCG 257
 QY 41 GlnLeuArgGlnArgGlnValValAspLeuTyrAsnGlyMetCysLeuGlnGlyProAla 60
 DB CAGCTCCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 317
 QY 61 GlyValProGlnArgGlnGlySerProGlyAlaAsnValIleProGlyTyrProGlyIle 80
 DB GGAGTGGCTGTGTGAACCGGAGCCCTCGGCGCAATGTTATTCGGGTACACCTGGAGTC 377
 QY 81 ProGlyArgGlnGlyLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100
 DB 378 CAGGTCGGGATGATTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 437
 QY 101 SerTyrThrProAsnTyrIleGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 120
 DB 438 TCCTGGACACCCAACTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 497
 QY 121 GlyLeuIleAlaGlnCysThrPheThrIleMetArgSerAsnSerAlaLeuArgValLeu 140
 DB 498 GGGAAATGCGGAGTGCATTTACAAAGATGCTTCAATAGCTTCAAGGAGTTTG 557
 QY 141 PheSerGlySerLeuArgLeuGlyCysArgAsnAlaCysCysGlnArgTyrPheThr 160
 DB 558 TTCAGTGGCTCACTTCGCTAAATGAGAAATGCAATGCTGCTGCTGCTGCTGCTGCTGCT 617
 QY 161 PheAsnGlyAlaGlnCysSerGlyProLeuProIleGlnAlaIleIleTyrLeuAspGln 180
 DB 618 TTCATGAGCTGAAATGTTACAGACCTTCCCTTAACCTTAATTTATTGAGCAAA 677
 QY 181 GlySerProGlnMetAsnSerThrIleAsnIleHisArgHisSerValGlnGlyLeu 200
 DB 678 GGAAGCCCGAAATGAATTCACAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 737
 QY 201 CysGlnGlyIleGlyAlaGlyLeuValAspValAlaIleTyrValGlyTyrCysSerAsp 220
 DB 738 TGTGAAGGAATGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 797
 QY 221 TyrProGlyAlaAspAlaSerThrGlyTyrAsnSerValSerArgIleIleIleGlnGln 240
 DB 798 TACCAAAAGAGATGCTTCTTCACTGAGTGAATTCAGTTTCTGCAATCATTTAGAAAGA 857

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 PR 24-JUL-1998; 98US-0094006P.
 PR 04-AUG-1998; 98US-0095282P.
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 PR 10-AUG-1998; 98US-0096012P.
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Alignment Scores:

Pred. No.: 2,55e-104 Length: 1257
 Score: 1301.00 Matches: 243
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 8 Gaps: 0

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 DB 198 CTGCTGACAGCTGCCGCCCGCTCGAGCGCTCTAGATCCCAAGGGAAGCAAGCGC 257
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 DB 318 GGAAGTCTGTGTCCAGACGAGAGCCCTGGGGCCAAATGTATTCGGGTACACCTGGGATC 377
 QY 81 ProGlyArgAspGlyPheLeuGlyGlyGluGlyCysLeuArgGInSerPheGInGlu 100
 DB 378 CCAGGTCCGGATGATTCATTAAGAGAAAGGGGAATGTGAGGGAACCTTGAGAG 437
 QY 101 SerThrProAsnTyrIleGInCysSerTyrSerSerLeuAnTyrGlyIleAspLeu 120
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 DB 618 TTCATGAGAGCTGATTTTCAGACCTCTTCCATTGAAGCTTATATTTAGACCA 677
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 QY 201 CysGluGlyIleGlyAlaGlyLeuValaIaIaIleTyrValGlyThrCysSerAsp 220
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 QY 221 TyrProGlyGlyAspAlaSerThrGlyTyrPAnSerValSerArgIleIleIleGluGlu 240
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 KM tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
 KM tissue typing; adrenal tumour; lung tumour; colon tumour; breast tumour;
 KM prostate tumour; rectal tumour; cervical tumour; liver tumour.
 OS Homo sapiens.
 OS US2003040060-A1.
 PN 27-FEB-2003.
 PD 24-JUN-2002; 2002US-00179525.
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Alignment Scores:

Pred. No.: 2,55e-104
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 Best Local Similarity: 100.00%
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 Gaps: 0

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 DB 198 CTGCTGCAAGCTCCGCGCGCTCGAGCGCTCTGAGATCCCAAGAGGAGCAAAAGCG 257
 QY 41 GlnLeuArgGlnArgGlnAlaValAlaPleuArgGlyMetCysLeuGlnGlyProAla 60
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 DT 28-AUG-2003 (first entry)
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 KW Human; gene; ss; secreted and transmembrane protein; PRO; TNF-alpha;
 KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
 KW tissue typing; adrenal tumour; lung tumour; colon tumour; breast tumour;
 KW prostate tumour; rectal tumour; cervical tumour; liver tumour.
 OS Homo sapiens.
 XX
 FN US2003044916-A1.
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 PD 06-MAR-2003.
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 PF 20-JUN-2002; 2002US-00176484.
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PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101739P.
PR 24-SEP-1998; 98US-0101743P.
PR 24-SEP-1998; 98US-0101922P.
PR 25-SEP-1998; 98US-0101922P.
PR 25-SEP-1998; 98US-0101786P.
PR 29-SEP-1998; 98US-0102207P.
PR 29-SEP-1998; 98US-0102240P.
PR 29-SEP-1998; 98US-0102330P.
PR 29-SEP-1998; 98US-0102331P.
PR 30-SEP-1998; 98US-0102487P.

PR 30-SEP-1998; 98US-0102570P.
 PR 30-SEP-1998; 98US-0102571P.
 PR 01-OCT-1998; 98US-0102684P.
 PR 01-OCT-1998; 98US-0102687P.
 PR 02-OCT-1998; 98US-0102965P.
 PR 06-OCT-1998; 98US-0103258P.
 PR 06-OCT-1998; 98US-0103449P.

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US-10-063-734-122 (1-243) x ACD18725 (1-1257)

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QY      21 LeuLeuGlnLeuProAlaProSerSerAlaSerGlnLeuProLysGlyLysGlnLysAla 40
DB      198 CTGCTGAGCTGCGCCCGCGCTGAGGCTCTGAGATCCCAAGGGGAGCAAAAGCGG 257
QY      41 GlnLeuArgGlnArgGlnValValAspLeuTyrAsnGlyMetCysLeuGlnGlyProAla 60
DB      258 CAGCTCCGGAGAGGAGGTGTGACCTGTATATGAAATGTGCTTACAGGGCCAGCA 317
QY      61 GlyValProGlyValArgAspGlySerProGlyValAsnValIleProGlyThrProGlyIle 80
DB      318 GAGATCCTGCTGAGAGCGGAGCCCTGGGGCCAATGTATTCGGGTACACCTGGGATC 377
QY      81 ProGlyArgAspGlyPheLysGlyGlyLysGlyLysGlyLysGlyLysGlyLysGlyLys 100
DB      378 CCAGTCGGGATGATTCAAAGAGAAAGGGGAATGTCTAGGAAAGCTTTGAGAG 437
QY      101 SerTyrThrProAsnTyrLysGlnCysSerTyrSerSerLeuAsnTyrGlyIleAspLeu 120
DB      438 TCTTGACACCCCAACACACAGAGGCTTCATGATGATTCATTAATGACATAGATCTT 497
QY      121 GlyLysIleAlaGlyCysThrPheThrLysMetArgSerAsnSerAlaLeuArgValLeu 140
DB      498 GGGAAATTGCGGAGGTGATTTACAAAGATGCGTTCAAAATAGTGTCTTAAGAGTTTG 557
QY      141 PheSerGlySerLeuArgLeuLysCysArgAsnAlaCysCysGlnArgTyrPheThr 160
DB      558 TTCAGTGGCTCACTTCGGCTAAATGCAAGAAATGCAATGCTGTCAAGCTTGATTTTCA 617
QY      161 PheAsnGlyAlaGlyCysSerGlyProLeuProIleGlnAlaIleIleTyrLeuAspGln 180
DB      618 TTCATGAGACTGAATGTTCAGACCTCTCCCATTTGAAGCTAATTAATTTATTTGACCAA 677
QY      181 GlySerProGlnMetAsnSerThrIleAsnIleHisArgThrSerSerValGlnGlyLeu 200
DB      678 GGAAGCCCTGAATGAATTCACCAATTAATATTCATCCACTTCTTCTGTGAAAGACTT 737
QY      201 CysGlnGlyIleGlyAlaGlyLeuValAspValAlaIleTyrValGlyThrCysSerAsp 220
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QY      241 LeuProLys 243
DB      858 CTACCAAAA 866

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Search completed: December 25, 2004, 05:43:48
 Job time : 511 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 25, 2004, 05:33:57 ; Search time 3198 Seconds
(without alignments)
2768.873 Million cell updates/sec

Title: US-10-063-734-122

Perfect score: 1301

Sequence: 1 MRPOGPASPRRLRLGLLL.....GDASNGMSVSRRIIEELPK 243

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Command line parameters:
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-DB=EST -QFMT=fasta -SUFFIX=rest -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bites -START=1 -END=1 -MATRIX=blosum62 -TRANS=human4.cdi -LIST=100
-DOCALLIGN=200 -THR SCORE=Pct -THR MAX=100 -THR MIN=0 -ALIGN=50 -MODE=LOCAL
-OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10063734@cgn2_1_13437@runat_22122004_101734_8933 -NCPU=6 -ICPU=3
-NO WMAP -LARGEDUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_est3: *
4: gb_est4: *
5: gb_est5: *
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7: gb_est7: *
8: gb_est8: *
9: gb_est9: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1294	99.5	732	9	AY399084 Homo sapi
2	1294	99.5	1103	3	CR594803 full-length
3	1294	99.5	1189	3	CR596030 full-length
4	1294	99.5	1207	3	CR605392 full-length
5	1289	99.1	1111	3	CR612318 full-length
6	1284	98.7	1288	3	BC021025 Homo sapi
7	1272	97.8	732	9	AY399085 Pan trogl
8	1267	97.4	827	1	AL544722 AL544722
9	1266	97.3	1100	1	AL551834 AL551834

10	1260	96.8	1132	4	BM560093
11	1254	96.4	1098	4	AL532456
12	1248	96.9	986	5	BX387691
13	1226	94.2	710	3	CR592899
14	1207	92.8	849	6	CB201936
15	1205	92.6	738	9	AY399086
16	1201	92.3	1161	3	AK003674
17	1195	91.9	716	6	CA413294
18	1181	90.8	1168	3	AK076498
19	1174	90.2	709	1	AL553798
20	1153.5	88.7	707	5	BX386416
21	1145.5	88.0	790	4	BI108785
22	1138	87.5	670	5	BX386415
23	1137	87.4	671	5	BU624465
24	1134	87.2	676	1	AL553771
25	1122	86.2	922	5	BQ425098
26	1112	85.5	654	5	BU624261
27	1106.5	85.0	1037	4	BM915926
28	1105	84.9	851	5	BQ425266
29	1104	84.9	1102	1	AL575307
30	1093	84.0	1064	1	AL564395
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32	1033	79.4	617	5	BQ574527
33	1019.5	78.4	986	5	BQ648112
34	1013	77.9	890	1	AL585129
35	1009.5	77.6	669	5	CU394776
36	993	76.3	700	7	CU394776
37	990.5	76.1	765	5	BU408973
38	970.5	74.6	681	5	BU278868
39	970.5	74.6	798	6	CB959810
40	952	73.2	570	5	BX265931
41	951.5	73.1	858	5	BU128948
42	951.5	71.1	995	5	BU141753
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44	930	71.5	638	5	BU257159
45	917.5	70.5	790	5	BX884616
46	917	70.5	571	7	CU394775
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48	906	68.6	902	5	BQ424201
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52	896	68.9	814	6	CB991371
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54	878	66.8	728	7	CR689549
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56	868	66.7	534	5	BX517433
57	865	66.3	508	5	BU700520
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59	846	65.0	676	5	BU326094
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63	824	63.3	666	2	CO696082
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BU270206	603509637
CR408276	CR408276
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      87      680      52.3      386      1      AU695311      AU695311
      88      676      52.0      963      7      CF376690      AGENCOURT
      89      674      51.8      513      7      CF359477      819240      MA
      90      674      51.8      655      6      CB197831      AGENCOURT
      91      670.5      51.3      583      4      BJ490431      BU490431
      92      667      51.3      542      6      BJ498080      BU498080
      93      662      50.9      744      4      CD741549      UI-M-A00-
      94      649      49.9      359      5      BX924504      BX924504
      95      643      49.4      399      5      BX924504      BX924504
      96      640      49.2      387      1      AA335862      BX924504
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ALIGNMENTS

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DEFINITION Homo sapiens CTRC1 gene, VIRUAL TRANSCRIPT, partial sequence,
ACCESSION  AY399084
VERSION     AY399084.1 GI:39755073
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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REFERENCE
AUTHORS    Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
            Todd,M.A., Tanenbaum,D.M., Civeille,D.R., Lu,F., Murphy,B.,
            Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Smitsky,J.D.,
            Adams,M.D. and Cargill,M.
            Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
            JOURNAL Science 302 (5652), 1960-1963 (2003)
            PUBMED 14671392
            2 (bases 1 to 732)
            Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
            Todd,M.A., Tanenbaum,D.M., Civeille,D.R., Lu,F., Murphy,B.,
            Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Smitsky,J.D.,
            Adams,M.D. and Cargill,M.
            Direct Submission
            Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
            This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
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ORIGIN

Alignment Scores:

Pred. No.:	2,12e-113	Length:	732
Score:	1294.00	Matches:	242
Best Local Similarity:	99.59%	Conservative:	0
Best Local Similarity:	99.59%	Mismatches:	1
Query Match:	99.46%	Indels:	0
DB:	9	Gaps:	0

US-10-063-734-122 (1-243) x AY399084 (1-732)

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      1 ATGCGACCCCGAGGCGCGCGCGCTCCCGAGGCGGCTCCGCGCTCTGCTCTCTG 60
      21 LeuLeuGInLeuProAlaProSerSerAlaSerGluLeuProGlyGlyGlyGly 40
      61 CTGCTGACGCTGCGCGCGCGCTGAGCGCTCTGAGATGCCCAAGGGAAGGAGGCG 120
      41 GInLeuArgGInArgGluValAlaAspleuTyZasnGlyMetCysLeuGInGlyProAla 60
      121 CAGCTCCGCGAGAGGAGGAGTGTGAGCTGTGATTAATGATGCTTACAGGCGCGCA 180
      61 GlyValPProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
      181 GAGAGTCCCTGCTGACAGCGGAGCGCTGGGCGCAATGAGCATTCGGGTACCTGGGATC 240
      81 ProGlyArgAspGlyPheLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100
      241 CCGAGTCCGAGTGTGATTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
      101 SerThrProAsnTyTyGInCysSerTyrSerSerLeuAsnTyTyGlyIleAspleu 120
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      121 GlyValIleAlaGluCysThrPheThrIleMetArgSerAsnSerAlaLeuArgValleu 140
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      481 TTCATGAGCTGAATGTGATGAGACCTCTCCATGAGCATATTAATTTATGAGCA 540
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      241 LeuProIys 243
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RESULT 2
LOCUS      CR594803      1103 bp      mRNA      linear      HTC 21-JUN-2004
DEFINITION Full-length cDNA clone CS0D1022YF04 of Placenta Cot 25-normalized
            of Homo sapiens (human).
ACCESSION  CR594803
VERSION     CR594803.1 GI:50475610
KEYWORDS    HTC; CNSLT; cDNA.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1103)
AUTHORS    Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE      Full-length cDNA libraries and normalization
JOURNAL    Unpublished
CONTACT    : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
            Faraday Avenue
            2 (bases 1 to 1103)
REFERENCE  Genoscope.
AUTHORS

```

TITLE Direct Submission
JOURNAL Submitted (20-JUN-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 Evry cedex - FRANCE (E-mail : sequef@genoscope.cns.fr

COMMENT - Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo (dt) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

FEATURES
source Location/Qualifiers
1..1103

/organism="Homo sapiens"
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/db_xref="taxon:9606"
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ORIGIN

Alignment Scores:

Pred. No.: 3,69e-113 Length: 1103
Score: 1294.00 Matches: 242
Percent Similarity: 99.59% Conservative: 0
Best Local Similarity: 99.59% Mismatches: 1
Query Match: 99.46% Indels: 0
Gaps: 0

US-10-063-734-122 (1-243) x CR594803 (1-1103)

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OY 21 LeuLeuGlnLeuProAlaProSeSerAlaSerGlnLeuProGlyGlyGlnYala 40
DB CTGCTGACAGCTCCCGCGCGCTGAGCGCGCTGAGATCCCAAGGGAAGCAAGGCG 189
OY 41 GlnLeuAArgGlnAArgGlnValAaLeuLeuYraAnglYmerCyLeuGlnGlnYProAla 60
DB CAGCTCCGCGCAGAGGAGGAGGTGTGACCTGTATATGAGATGTCTTACAAAGGCGCAGCA 249
OY 190 GAGTCCGCGCAGAGGAGGAGGTGTGACCTGTATATGAGATGTCTTACAAAGGCGCAGCA 249
OY 61 G1YValProglYArGArpGlySerProglYAlaAenValIleProglYThrProglYIle 80
DB GGAAGTCCCTGCTGAGACCGGAGCCCTGGGCGCAATGCAATCCGGGTACACTGGAGATC 309
OY 250 GGAAGTCCCTGCTGAGACCGGAGCCCTGGGCGCAATGCAATCCGGGTACACTGGAGATC 309
OY 81 ProglYArGArpGlyPheLysGlyGlnYGlnCyLeuAArgGlnSerPheGlnGln 100
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DB TCCTGAGACCCCAACACAGACGAGTGTATGAGATGTCTTGAATTAATGCAATGATCTT 429
OY 121 G1YValIleAlaGlnCySerThrPheThrYmerArGArpSerAlaLeuAArgValLeu 140
DB GGGAAATATGCGGAGGTGATCATTTACAAAGATGCGTTCAAATAGTCTCTTAAGAGTTTG 489
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OY 161 PheAenGlnYAlaGlnCySerGlyProLeuProIleGlnAlaIleIleYrLeuAArgGln 180
DB TTCAATGAGAGTGAATGTTCAAGACCTCTTCCATTTGAAGCTAATTAATTTTGAACCAA 609
OY 181 G1YSerProglYmerAenSerThrIleAenIleAenIleAenIleAenIleAenIleAen 200
DB GGAAGCCCTGAATGATTCACAAATTAATTAATTCACGACCTTCTCTGAGAGGACATT 669
OY 201 CyGlnGlyYrIleG1YAlaGlnYLeuValAaPValAlaIleTPYAlaGlyYrCySerAaP 220
DB TGTGAAGAAATGCTGCTGATTAAGTGAATGTTGATCTATCTGGGTGTACTGTTCAAGAT 729

OY 221 TyrProLysGlyAaPAlaSerThrGlyYrPaAenSerValSerArgIleIleIleGlnGln 240
DB TACCAAAAGAGATGCTTCTACTGATGATGATGATGATGATGATGATGATGATGATGATG 789

OY 241 LeuProLys 243
DB CTACCAAAA 798

RESULT 3

LOCUS

CR596030 1189 bp mRNA linear HTC 21-JUN-2004

DEFINITION full-length cDNA clone CSODI061YA20 of Placenta Cot 25-normalized of Homo sapiens (human).

ACCESSION

CR596030.1 GI:50476837

KEYWORDS

HTC; CDSUT_cDNA.

SOURCE

ORGANISM

REFERENCE

AUTHORS

JOURNAL

COMMENT

FEATURES

source

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI061YA20"
/issue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"

ORIGIN

Alignment Scores:

Pred. No.: 4,09e-113 Length: 1189
Score: 1294.00 Matches: 242
Percent Similarity: 99.59% Conservative: 0
Best Local Similarity: 99.59% Mismatches: 1
Query Match: 99.46% Indels: 0
Gaps: 0

US-10-063-734-122 (1-243) x CR596030 (1-1189)

OY 1 MetatgProglnglYProAlaAaSerProglnglYleuLeuLeuLeu 20
DB ATGCCAAGCCAGGAGGCGCGCGCTCCCGCAGCGGCTCCGCGCTCTGCTGCTCTG 153
OY 94 ATGCCAAGCCAGGAGGCGCGCGCTCCCGCAGCGGCTCCGCGCTCTGCTGCTCTG 153
OY 21 LeuLeuGlnLeuProAlaProSeSerAlaSerGlnLeuProGlyGlyGlnYala 40
DB CTGCTGACAGCTCCCGCGCGCTGAGCGCGCTGAGATCCCAAGGGAAGCAAGGCG 213
OY 154 CTGCTGACAGCTCCCGCGCGCTGAGCGCGCTGAGATCCCAAGGGAAGCAAGGCG 213
OY 41 GlnLeuAArgGlnAArgGlnValAaLeuLeuYraAnglYmerCyLeuGlnGlnYProAla 60
DB CAGCTCCGCGCAGAGGAGGAGGTGTGACCTGTATATGAGATGTCTTACAAAGGCGCAGCA 273
OY 214 CAGCTCCGCGCAGAGGAGGAGGTGTGACCTGTATATGAGATGTCTTACAAAGGCGCAGCA 273
OY 61 G1YValProglYArGArpGlySerProglYAlaAenValIleProglYThrProglYIle 80
DB GGAAGTCCCTGCTGAGACCGGAGCCCTGGGCGCAATGCAATCCGGGTACACTGGAGATC 333
DB 274 GGAAGTCCCTGCTGAGACCGGAGCCCTGGGCGCAATGCAATCCGGGTACACTGGAGATC 333

Oy		1	ProgliaCABPGLyPhbLyGlyLylusgLygtUcYLeuaArgIuseRpheluglu	100
Dd		334	CAGGTCCGGATGGATTGAATAAGGAGAAAAAGGGGAAAGTCTCGAAGGAAACGTTTGAGAG	393
Oy		101	SerTPThrProAsnTYLYeGLInCysSerTrpSerSerLeuAenTYRGlylleaspLeu	120
Dd		394	TCTTCGACACCACCACTACACAGAGGTTCATGAGACTTCATTAATTCGCATRGACTT	453
Oy		121	GlyysilleaGluCyseThrPhethLlysMelaArgSerAnsSeraaleuaArgvalleu	140
Dd		454	GGGAAAATTGCCGGAGTGACATTTACAAAGATGGCTTCAAATAGTCTTAAGAGTTTG	513
Oy		141	PheSerGlySerLeuAArgLeuLysCYArGAsnAlaCYsCySGlnAqTRpyrpHeThr	160
Dd		514	TTCAGTGCTCACCTTCGGCTAAATATGAGAAtGCAATGCTCTCAGCCTTGATTCACA	573
Oy		161	PhaaSnGlylaGluCyseSerGlyProLeuProileGualalleyleTyLeaapGln	180
Dd		574	TTCAATGAGACTGATATGATTGACAGCCTTCCTCCAATGAACTTAAATTTATTTGACCA	633
Oy		181	GlySerProGluMetAsnSerthrilleasnilleharGthSerSerValGluGlyLeu	200
Dd		634	GGAAGCCCTGAATGAATTCACACTTAATTCATGCACTTCTTGtGGAAGACTT	693
Oy		201	CySGlGlyllleGlyValaglyLeuValAspValalleTrpValglyThrCyseAsp	220
Dd		694	TGTGAAGAAATGTGCTGATTNAGGAAGTGTCACTGAGGTTGTGACTTGTTCAAT	753
Oy		221	TYRProLysGlyAspaLaSerThrglyTYRPAnSerValSerArglllelleGluGlu	240
Dd		754	TACCCAAAAGAGATGCTCTTACTGATGAAATTCAGTTTCGCAATCATTTATGAAGA	813
Oy		241	LeuProLys	243
Dd		814	CTAACAAAA	822
RESULT 4				
LOCUS	CR605392			
DEFINITION	full-length cDNA clone CS0D1037YD19 of Placenta Cot 25-normalized			
ACCESSION	CR605392			
VERSION	CR605392.1			
KEYWORDS	HTC; CNSLT; cDNA.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
TITLE	1. (bases 1 to 1207)			
JOURNAL	L.I.W.B., Gruber,C., Jessee,J. and Polayes,D.			
REMARK	Full-length cDNA libraries and normalization			
	Unpublished			
	Contact : Feng Liang Email : fliang@life.techn.com URL :			
	http://fulllength.invitrogen.com/ Invitrogen Corporation 1600			
	Paradey Avenue			
	2 (bases 1 to 1207)			
	Genoscope.			
REFERENCE	Direct Submission			
AUTHORS	Submitted (20-JUL-2004) Genoscope - Centre National de Sequenage :			
TITLE	BP 191 91006 EVRY cedex - FRANCE (E-mail : segre@genoscope.cns.fr			
JOURNAL	- web : www.genoscope.cns.fr)			
	1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime			
	into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library			
	was normalized. Library was constructed by Life Technologies, a			
	division of Invitrogen.			
FEATURES	location/Qualifiers			
source	1..1207			
	/organism="Homo sapiens"			
	/mol_type="mRNA"			
	/db_xref="taxon:9606"			
	/clone="CS0D1037YD19"			

ALIGNMENT SCORES:	4.17e-113	Length:	1207
Pred. No.:	1294.00	Matches:	242
Score:	99.59%	Conservative:	0
Percent Similarity:	99.59%	Mismatches:	1
Best Local Similarity:	99.59%	Indels:	0
Query Match:	99.46%	Gaps:	0
DB:	3		
US-10-063-734-122 (1-243) x CR605392 (1-1207)			
QY	1 MetArgProGlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeuLeu 20		
DB	94 ATCGACCCACAGAGGCCCGCCCGCTCCCGCAGCGGCTCCGCGGCTCTGCTCTCG 15		
QY	21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluLeuProGlyGlyGlnGlyAla 40		
DB	154 CTGCTGACACTCCCGCCCGCTCCAGCGCTCTGAGATCCCAAGGAGGACAAAGGCG 21		
QY	41 GlnLeuArgGlnArgGlnValValAlaSerLeuThrArgGlyMetCysLeuGlnGlnProAla 60		
DB	214 CAGCTCCGCGACAGAGGAGAGTGTGACCTGTTATTAAGAAATGCTTACAAAGGCGACGA 272		
QY	61 GlyValProGlyValArgAspGlySerProGlyValAlaAlaValIleProGlyThrProGlyIle 80		
DB	274 GGAAGTCCGTGTCGACGCGGAGCCCTGAGGCGCAATGGCAATTCGGGATTCACCTGGATC 333		
QY	81 ProGlyArgAspGlyPheLeuGlyGlyValGlyGlyCysLeuArgGlySerPheGlnGlu 100		
DB	334 CCAAGTCCGGATGATTCATTAAGAGAAAGGGGAATGTCTAAGGAAAGCTTTGAGGAG 393		
QY	101 SerTyrThrProAlaGlyValGlyGlnCysSerTyrSerSerLeuAlaGlyIleAspLeu 120		
DB	394 TCTTGAGACACCACTACAGACAGTGTTCATGAGATTCATGAATTAAGCATAGATCTT 453		
QY	121 GlyValIleAlaGluCysThrPheThrIleMetArgSerSerAlaLeuArgValLeu 140		
DB	454 GGGAAATTTGGCGAGTGTACATTTTACAAAGAGCGCTTCAAAATAGCTCTAAGAGTTTG 513		
QY	141 PheSerGlySerLeuArgLeuIleCysArgAlaAlaCysCysGlnArgTyrPheThr 160		
DB	514 TTCAGTGGCTCACCTCGGCTAAATCAGAAATGATGATGTCGACAGCTGTGATTTACA 573		
QY	161 PheAlaGlyValGluCysSerGlyProLeuProIleGluAlaIleIleIleTyrLeuAspGln 180		
DB	574 TTCATAGACTGAATGTTTCAAGACTCTTCCCATGTGAAGCTATTAATTTATTGGACCA 633		
QY	181 GlySerProGluLeuArgSerThrIleAlaGlnIleHisArgThrSerSerValGluGlyLeu 200		
DB	634 GGAAGCCCTGAATTAATGATTCACAAATATATATATATATGATTCCTTCTGAGGAGACTT 693		
QY	201 CysGlnGlyIleIleGlyValGlyLeuValAlaIleIleTyrValGlyIleCysSerAsp 220		
DB	694 TGTGAGAGATTTGTCTGTGATTTAGATGTGTCTGCTGGTGTGTACTTGTTCAGAT 753		
QY	221 TyrProIleGlyValAspAlaSerThrGlyTyrPheSerValSerArgIleIleIleGluGlu 240		
DB	754 TACCCAAAGAGAGATGCTCTTCACTGAGATGGAATTCAGTTTCTGCATCATTAATTGAAGA 813		
QY	241 LeuProIle 243		
DB	814 CTACCAAAA 822		
RESULT 5			
CR612318	1111 bp	mRNA	linear
LOCUS	full-length cDNA clone	CSDBM014YN20	Fetal liver of Homo sapiens
DEFINITION	(human)		
ACCESSION	CR612318		
VERSION	1		

KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REMARK

HTC; CNSLT_CDNA.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 1111)
Li, W.B., Gruber, C., Jesse, J., and Polayes, D.
Full-length cDNA libraries and normalized
Unpublished
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 1111)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
Location/Qualifiers
1. 1111
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DM014YN20"
/issue_type="Fetal liver"
/plasmid="pCMVSPORT_6"

ORIGIN

Alignment Scores:
Pred. No. : 1,12e-112 Length: 1111
Score: 1289.00 Matches: 241
Percent Similarity: 99.59% Conservative: 0
Best Local Similarity: 99.59% Mismatches: 1
Query Match: 99.08% Indels: 0
DB: Gaps: 0

US-10-063-734-122 (1-243) x CR612318 (1-1111)

QY 2 ATGPPGGLGlyProAlaIaSerProGlnArgLeuArgGlyLeuLeuLeuLeu 21
DB 2 CGACCCAGAGGCCCCCGCCCTCCCGCAGCGGCTCGCGCTCTGCTGCTGCTG 61
QY 22 LeuGlnLeuProAlaProSerSerAlaSerGluIleProGlyGlyGlyGlyGlyGly 41
DB 62 CTGCACCTGCGCGCGCGCTGACGCGCTCTGAGATCCCAAGGGAAGCAAGCAAGCGCAG 121
QY 42 LeuArgGlnArgGluValValAlaLeuLeuArgGlyGlyGlyGlyGlyGlyGly 61
DB 122 CTCGGCAGAGGAGGAGGTGTGACCTGTATATGATGATGCTTACAGGCGCAGAGCA 181
QY 62 ValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIlePro 81
DB 182 GTGCTGTGTGAGACGAGGAGCCCTGGGCGCCAAATGGCAATTCGGGTACACCTGGGATCCCA 241
QY 82 GAlArgAspGlyPheLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 101
DB 242 GGTCCGAGATGATTCAG 301
QY 102 TTTTThProAsnTyrLeuGlnCysSerTTPSerSerLeuAsnTyrGlyIleAspLeuGly 121
DB 302 TGGACACCAACATCAAGCAGTGTTCATGAGATTGATGATGATGATGATGATGATG 361
QY 122 TyeIIGAlGlnCysThrPheThrTyrMetArgSerAsnSerAlaLeuArgValIleAsp 141
DB 362 AAAATGCGAGAGTGCATTATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 421
QY 142 SerGlySerLeuArgLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 161

DB 422 AGTGGCTCACTTCGGCTAAATATGAGAAATGATGATGATGATGATGATGATGATGAT 481
QY 162 AAGGAlaIaGluCysSerGlyProLeuProIleGluAlaIleIleTyrLeuAspGlnGly 181
DB 482 AATGAGAGTGAATGTCAGAGACCTCTCCATGAGCTATATATATATATATATATATAT 541
QY 182 SerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGluGlyLeuGly 201
DB 542 AGCCCTGAATATATATCAACATTAATATATATATATATATATATATATATATATATAT 601
QY 202 GluGlyIleGlyAlaGlyLeuValAlaIleTTPValGlyThrCysSerAspTyr 221
DB 602 GAAGGAATTTGTCGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 661
QY 222 ProGlyArgAspAlaSerThrGlyTTPAsnSerValSerArgIleIleIleGluGluLeu 241
DB 662 CCAAAAGGAGATGCTTTCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 721
QY 242 ProGly 243
DB 722 CCNAAA 727

RESULT 6
BC021025 1288 bp mRNA linear HTC 04-AUG-2004
LOCUS
DEFINITION
Homo sapiens collagen triple helix repeat containing 1, mRNA (cDNA
clone IMAGE:3617432).
ACCESSION
BC021025
VERSION
BC021025.1 GI:16045042
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 1288)
Klausner, R.D., Collins, F.S., Wagner, C.M., Schuler, G.D.,
Altschuld, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carinici, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullihy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richard, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulik, S.N.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahy, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalek, U., Smalins, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 1288)
JOURNAL
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL

NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
Contact: cgabbs-remail.nih.gov
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DRP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
contact: amadansystemsbiology.org

Anup Madan, Jessica Fahey, Erin Helton, Mark Ketieman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/BLML at: <http://image.lhml.gov>
 Series: IRAL Plate: 24 Row: 1 Column: 7
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 19923988
 This clone has the following problem: no cloning site / microdeletion.

FEATURES
 source
 1..1288
 location/Qualifiers

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3617432"
 /cissue_type="Skin, melanotic melanoma."
 /clone_id="NIH MGC_20"
 /lab_host="DH10B-R"
 /note="Vector: pOT87"

ORIGIN

Alignment Scores:

Pred. No.: 4,12e-112 Length: 1288
 Score: 1284.00 Matches: 241
 Percent Similarity: 99.18% Conservative: 0
 Best Local Similarity: 99.18% Mismatches: 2
 Query Match: 98.69% Indels: 0
 DB: 3 Gaps: 0

US-10-063-734-122 (1-243) x BC021025 (1-1288)

1 MetATGProGlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeu 20
 143 ATGGACCCCAAGGGCCCGCCGCTCCGCGACGCGCTCCGCTGCTGCTCTG 202
 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGlnLeuProGlyGlyGlnGln 40
 203 CTGCTGACAGCTGCCCGCCGCTGACGCGCTCTGACATCCCAAGGGGAAAGGCG 262
 41 GlnLeuArgGlnArgGlnValValAlaPheLeuTYRAsnGlyMetCysLeuGlnGlyProAla 60
 263 CAGCTCCCGGACAGGAGGAGCTGGTGGACCTGTATTAATGGAATGCTTCAAGGGCCACGA 322
 61 GlyValProGlyArgAspGlySerProGlyValAsnValIleProGlyThrProGlyIle 80
 323 GGAAGTCCCTGTCGAGACGGAGCCCTGGGGCCAAATGGCAATCCGCGTACACCTGGGATC 382
 81 ProGlyArgAspGlyPheLeuGlyGlnGlyCysLeuArgGlySerPheGlnGln 100
 383 CCAGGTCCGGATGATTCAAAGAGAAAGGGGGAATGCTGAGGAAAGCTTTGAGGAG 442
 101 SerTPTrProAsnTYRLeuGlnCysSerTPSerSerLeuAsnTYRLeuAspLeu 120
 443 TCTTGACACCCCACTACAGAGAGTTCATGAGATTCATGAATTAATGATAGATCTT 502
 121 GlyTYRLeuAlaGlnCysThrPheThrTYRMetArgSerAsnSerAlaLeuArgValLeu 140
 503 GGGAAATTTGGAGTGAATTCATTAACAAGATGCTTCAATAGTCTTAAGAGATTTTG 562
 141 PheSerGlySerLeuArgLeuLeuGlyCysArgAsnAlaCysCysGlnArgTYRThrPheThr 160
 563 TTCAGTGGCTCACTTCGGCTAAATGAGAAATCATCTGTCGCGTGTATTTCACA 622
 161 PheAsnGlyAlaGlnCysSerGlyProLeuProIleGlnAlaIleIleTYRLeuAspGln 180
 623 TTCAATGAGAGCTGATGTTCCAGACCTCTTCCATGAGCTATAATTTATTGGACCAA 682
 181 GlySerProGlnMetAsnSerThrIleAsnIleHisArgThrSerSerValGlnGlyLeu 200
 683 GGAAGCCCTGAAATGAATTAACAATTAATATGACATCTTCTGCGAAGGACCTT 742
 201 CysGlnGlyIleGlyAlaGlyLeuValAspValAlaIleTPValGlyThrCysSerAsp 220

DB 743 TGTGAAGAAATGCGTGGATGATGATGATGATGATGATGATGATGATGATGAT 802
 QY 221 TYPProLYGlyAspAlaSerThrGlyTYRAsnSerValSerArgIleIleIleGlnGlu 240
 DB 803 TACCCAAATGAGATGCTTCTTACGAGATGAGATGAGATGAGATGAGATGAGATGAGAA 862
 QY 241 LeuProLYG 243
 DB 863 CTACCAAAA 871

RESULT 7
 AY399085
 LOCUS
 DEFINITION
 Pan troglodytes CTRH1 gene, VIRUAL TRANSCRIPT, partial sequence,
 genomic survey sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Pan troglodytes (chimpanzee)
 Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.

REFERENCE
 AUTHORS
 Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
 Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
 Perriera, S., Wang, G., Zheng, X.H., White, T.J., Shtinsky, J.J.,
 Adams, M.D., and Cargill, M.

TITLE
 Interfering nonneutral evolution from human-chimp-mouse orthologous
 gene trios

JOURNAL
 PUBLISHED
 REFERENCE
 AUTHORS
 Science 302 (5652), 1960-1963 (2003)
 14671302
 2 (bases 1 to 732)

TITLE
 Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
 Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
 Perriera, S., Wang, G., Zheng, X.H., White, T.J., Shtinsky, J.J.,
 Adams, M.D., and Cargill, M.

JOURNAL
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 This sequence was made by sequencing genomic exons and ordering
 them based on alignment.

COMMENT
 location/Qualifiers
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 /db_xref="taxon:9598"
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 /gene="CTHRC1"
 /locus_tag="HCN0106"

gene
 ORIGIN

Alignment Scores:

Pred. No.: 2.7e-111 Length: 732
 Score: 1272.00 Matches: 239
 Percent Similarity: 98.35% Conservative: 0
 Best Local Similarity: 98.35% Mismatches: 4
 Query Match: 97.77% Indels: 0
 DB: 9 Gaps: 0

US-10-063-734-122 (1-243) x AY399085 (1-732)

QY 1 MetATGProGlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeu 20
 DB 1 ATGGACCCCAAGGGCCCGCCGCTCCGCGACGCGCTCCGCTGCTGCTCTG 60
 QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGlnLeuProGlyGlyGlnGln 40
 DB 61 CTGCTGACAGCTGCCCGCCGCTGACGCGCTCTGACATCCCAAGGGGAAAGGCG 120
 QY 41 GlnLeuArgGlnArgGlnValValAlaPheLeuTYRAsnGlyMetCysLeuGlnGlyProAla 60
 DB 121 CAGCTCCGGACAGGAGGAGCTGGTGGACCTGTATTAATGGAATGCTTCAAGGGCCACGA 180


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QY 61 G1yValPProG1yARgAspG1ySerProG1yAlaAsnVal11leProG1yThrProG1yIle 80
DB 181 GGAGTGCCTGCTGACGACGGAGCCCTGGGCGCAATGCAATTCGGGTACACCTGGGATC 240
QY 81 ProG1yARgAspG1yPhe1ySg1yG1yG1yCylAsuArg1ySerPheG1yG1n 100
DB 241 CCAGGTGGGATGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
QY 101 SerTPThProAsnTy1ySg1yCySerTPSerSerLeuAsnTy1y11leAsp1eu 120
DB 301 TCCTGGACACCCCAACACACAGAGTGTTCATGAGTTCATGATTAATGATGATGATCTT 360
QY 121 G1yV11leAlaG1yCylSerThyPheThyMetArgSerAsnSerAlaLeuArgVal1eu 140
DB 361 GGGAAATTCGCGNNNNNTTCATTTACAAAGATCGCTTCAAGAGTCGNNNNAAGAGTTTG 420
QY 141 PheSerG1ySerLeuArgLeu1ySylAsnAlaCySylAsnArgTPThyPheThr 160
DB 421 TTCAGTGGCTCACTTCGGCTAAATGCAAGATGATGATGATGATGATGATGATGATGAT 480
QY 161 PheAsnG1yAlaG1yCylSerG1yProLeuPro11leG1yAla11le1y1y1y1y1y1y1y 180
DB 481 TTCATGAGGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
QY 181 G1ySerProG1yMetAsnSerThy11leAsn11le1y1y1y1y1y1y1y1y1y1y1y1y 200
DB 541 GGAAGCCCTGGAATGATTCACAAATTAATTCATGATGATGATGATGATGATGATGATGAT 600
QY 201 CySg1yG1y11leG1yAlaG1yLeuValAspValAla11leTPyAlaG1yThyCySylAsp 220
DB 601 TGTGAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
QY 221 TyTPro1yG1yAspAlaSerThyG1yTPAsnSerValSerArg11le11le1y1y1y1y1y 240
DB 661 TACCCAAAAGAGATGCTTCTACTGATGATGATGATGATGATGATGATGATGATGATGAT 720
QY 241 LeuPro1yS 243
DB 721 CTACCAAAA 729
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RESULT 8
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LOCUS AL544722 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION c1one CS0D1022YF04 5-PRIME, mRNA sequence.
ACCESSION AL544722
VERSION AL544722.3 GI:45745219
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 827)
Li,W.B., Gruber,C., Jesse,J., and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:3126563.
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segefe@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by life technologies, a
division of invitrogen. This sequence belongs to sequence cluster
4941.f
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For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?b=CS0D1022C020P1c=4941.f.
Location/Qualifiers
1. .827
/organism="Homo sapiens"

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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1022YF04"
/issue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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ORIGIN

Alignment Scores:

Pred. No.:	9,586-111	Length:	827
Score:	1267.00	Matches:	241
Percent Similarity:	99.18%	Conservative:	0
Best Local Similarity:	99.18%	Mismatches:	2
Query Match:	97.39%	Indels:	1
DB:	1	Gaps:	0

US-10-063-734-122 (1-243) x AL544722 (1-827)

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QY 1 MetArgProG1yG1yProAlaAlaSerProG1yAlaArg1yLeuLeuLeuLeu 20
DB 70 ATGCCACCCACAGGCGCCGCCCTCCCGACGCGCTCCGGGCGCTCTGCTCTCTG 129
QY 21 LeuLeuG1yLeuProAlaProSerSerAlaSerG1y11lePro1yG1y1ySg1y1ySg1yAla 40
DB 130 CTGCTGACGCTCCCGCGCGCGCTCGAGCGCTCTGAGATCCCAAGGAGAGAGAGAGAG 189
QY 41 G1yLeuArg1yG1yAlaValAlaAspLeuTy1yAsnG1yMetCySylAsnG1yProAla 60
DB 190 CAGTC-CGGCAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 248
QY 61 G1yValPProG1yARgAspG1ySerProG1yAlaAsnVal11leProG1yThrProG1yIle 80
DB 249 GGAGTGCCTGCTGACGACGGAGCCCTGGGCGCAATGCAATTCGGGTACACCTGGGATC 308
QY 81 ProG1yARgAspG1yPhe1ySg1yG1yG1yCylAsuArg1ySerPheG1yG1n 100
DB 309 CCAGGTGGGATGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 368
QY 101 SerTPThProAsnTy1ySg1yCySerTPSerSerLeuAsnTy1y11leAsp1eu 120
DB 369 TCCTGGACACCCCAACACAGAGTGTTCATGAGTTCATGATTAATGATGATGATGATGAT 428
QY 121 G1yV11leAlaG1yCylSerThyPheThyMetArgSerAsnSerAlaLeuArgVal1eu 140
DB 429 GGGAAATTCGCGNNNNNTTCATTTACAAAGATCGCTTCAAGAGTCGNNNNAAGAGTTTG 488
QY 141 PheSerG1ySerLeuArgLeu1ySylAsnAlaCySylAsnArgTPThyPheThr 160
DB 489 TTCAGTGGCTCACTTCGGCTAAATGCAAGATGATGATGATGATGATGATGATGATGATGAT 548
QY 161 PheAsnG1yAlaG1yCylSerG1yProLeuPro11leG1yAla11le1y1y1y1y1y1y1y 180
DB 549 TTCATGAGGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 608
QY 181 G1ySerProG1yMetAsnSerThy11leAsn11le1y1y1y1y1y1y1y1y1y1y1y1y 200
DB 609 GGAAGCCCTGGAATGATTCACAAATTAATTCATGATGATGATGATGATGATGATGATGAT 668
QY 201 CySg1yG1y11leG1yAlaG1yLeuValAspValAla11leTPyAlaG1yThyCySylAsp 220
DB 669 TGTGAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 728
QY 221 TyTPro1yG1yAspAlaSerThyG1yTPAsnSerValSerArg11le11le1y1y1y1y1y 240
DB 729 TACCCAAAAGAGATGCTTCTACTGATGATGATGATGATGATGATGATGATGATGATGAT 788
QY 241 LeuPro1yS 243
DB 789 CTACCAAAA 797
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RESULT 9
AL551834 1100 bp mRNA linear EST 30-MAR-2004
LOCUS AL551834 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS001061A20 5-PRIME, mRNA sequence.
ACCESSION AL551834
VERSION AL551834.3 GI:45856624
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1100)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:31273650.
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
4941.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?c=CS001061A20P1c=4941.f.
FEATURES
source
1..1100
location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS001061A20"
/issue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized." sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
Alignment Scores:
Pred. No.: 1,76e-110 length: 1100
Score: 1266.00 Matches: 241
Percent Similarity: 99.18% Conservative: 0
Best Local Similarity: 99.18% Mismatches: 2
Query Match: 97.31% Indels: 1
Gaps: 0
US-10-063-734-122 (1-243) x AL551834 (1-1100)
QY 1 MetAagProGInGlyProAlaAlaSerProGInaTgLeuAgtGlyLeuLeuLeuLeu 20
Db 94 ATGCACCCCGAGGCGCCCGCCGCTCCCGCGAGCGGCTCCGGGCGCTCTGCTCTCTG 153
QY 21 LeuLeuGInLeuProAlaProSerSerAlaSerGInLeuProGlyGlyGInLeuA 40
Db 154 CTGCTGCGAGCTGCCCGCCCGCTCGAGCCCTCTGAGATCCCAAGGGGAGCAAAAGCG 213
QY 41 GInLeuAgtGInaTgLeuAlaValaAspLeuTyraAnglyMetCysLeuGInGlyProAla 60
Db 214 CA-CTCCGGCAGAGGAGAGTGTGGACCTGTATATGAAATGCTTCAAGGGCGAGCA 272
QY 61 GlyValProGlyAaGAspGlySerProGlyAlaAbnValIleProGlyThrProGlyIle 80
Db 273 GGAAGTCCGTGTCAGACGAGGAGCCCTGGGGCCCAATGTCATTCGGGTACACCTGGGATC 332
QY 81 ProGlyAaGAspGlyPheTyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100
Db 333 CCAAGTCCGAGATGATTCAAAGAGAAAGGGGAGAAATGTCAGAGGAGAAAGCTTTGAGAG 392

QY 101 SerTTPThProAsnTyrlYsGInCysSerTTPSerSerLeuAsnTyrlYsAspLeu 120
Db 393 TCTTGAGACCCCACTACAGAGAGTCTTCAGAGCTTCATTAATTAAGCAATAGACTT 452
QY 121 GlyIysIleAlaGlyCysThrPheThrIysMetArSerArSerArSerAlaLeuAgtVal 140
Db 453 GGGAAATATGCGAGATGTACATTTACAAAGATGCGTCAATATGTCCTTAAGAGTTTG 512
QY 141 PheSerGlySerLeuAgtLeuTyGAspGlnaCysGlnaCysGlnaGlyGlyGlyGly 160
Db 513 TTCAGTGGTCACTTCGGCTTAATGCAAGATGCAATGCTGAGCGTGTGATTTTCA 572
QY 161 PheAnglyAlaGlyCysSerGlyProLeuProIleGlnaIleIleIleTyrlYsAspGln 180
Db 573 TTCATGTAGAGCTGATGTTCAGACCTTCCTCCCTTAAGCTATTAATTTATTTGAGCA 632
QY 181 GlySerProGlyMetArSerThrIleAsnIleHisArgThrSerSerValGlyGlyLeu 200
Db 633 GGAAGCCCTGAATGAATTTCAACATTAATTAATTCATGCACTTCTGTGAGAGACTT 692
QY 201 CysGInGlyIleGlyAlaGlyLeuValaAspValaIleTTPValGlyThrCysSerArp 220
Db 693 TGTGAAGGAATTTGGTGTGATTAAGTGAATGCTTCTGAGTGTGCACTTGTTGAGAT 752
QY 221 TyrProIysGlyAaPAlaSerThrGlyTTPArSerValSerArGlyIleIleIleGlyGlu 240
Db 753 TACCAAAAGAGATGCTTCTACATGATGATGATTCAGTTTCGTCATTTATTAAGAA 812
QY 241 LeuProIys 243
Db 813 CTACCAAAA 821

RESULT 10
LOCUS BMS60093 1132 bp mRNA linear EST 20-FEB-2002
DEFINITION AGENCOURT 6592628 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5476455
5', mRNA sequence.
ACCESSION BMS60093
VERSION BMS60093.1 GI:18804229
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1132)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-romail.nih.gov
Tissue Procurement: DCTD/DTP
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMNL at:
http://image.llnl.gov
plate: LNCM1992 row: o column: 16
High quality sequence stop: 638.
location/Qualifiers
1..1132
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5476455"
/issue_type="amelanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 41"
/note="Organ: skin; Vector: pOT87; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGGCGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,

FEATURES
source

Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.:	6,85e-110	Length:	1132
Score:	1260.00	Matches:	239
Percent Similarity:	97.95%	Conservative:	0
Best Local Similarity:	97.95%	Mismatches:	4
Query Match:	96.85%	Indels:	1
DB:	4	Gaps:	0

US-10-063-734-122 (1-243) x BMS60093 (1-1132)

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Qy      1 MetAATGProGlnGlyProAlaAlaSerProGlnAArgLeuArgGlyLeuLeuLeuLeu 20
Db      87 ATGCCAGCCCGAGGGCCCGCCGCTCCCGCAGCGGCTCCGCGCTCCGCTGCTCCG 146
Qy      21 LeuLeuGlnLeuProAlaProSerSerAlaSerGlnIleProArgGlyLeuGlnysAla 40
Db      147 CTGCTGACCTGCCCCCGCTGAGCCGCTCTGAGATCCCAAGGGGAAAGCAAGGGCG 206
Qy      41 GlnLeuArgGlnArgGlnValValAlaLeuLeuTyraGlnGlyMetCysLeuGlnGlyProAla 60
Db      207 CAGCTCCGCGCAGAGGAGGTGTGAGACTGTATATGATGATGCTTACAGAGGCGCAGCA 266
Qy      61 G1yValProG1yAArgAspG1ySerProG1yAlaAsnValIleProG1yThrProG1yIle 80
Db      267 GGAGTGCCTGTGTGAGACCGGAGCCCTCGGGCCAAATGCAATCCGGGTACCTCGGAGATC 326
Qy      81 ProG1yAArgAspG1yPheLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100
Db      327 CAGGTCGGAGATGATTCAGAGAGAAAGGGGAAATGTCTGAGGAAAGCTTTGAGGAG 386
Qy      101 SerTPThrProAsnTyrlsGlnCysSerTPSerSerLeuAsnTyrlsIleAspLeu 120
Db      387 TCCTGGACACCCAACTACAGAGAGGTGTATGATGATGATGATGATGATGATGATGAT 446
Qy      121 G1yValIleAlaG1ySerThrPheThrIleMetArgSerSerAlaLeuArgValLeu 140
Db      447 GGGAAATATGCGAGATGATTCATTTACAAAGATCGCTTCAATATGCTCTTAAGAGTTTG 506
Qy      141 PheSerG1ySerLeuArgLeuLysCysArgAsnAlaCysCysGlnArgTrpIlePheThr 160
Db      507 TTCAGTGGCTCACTTGGCTTAATATCAAGATGATGATGATGATGATGATGATGATGAT 566
Qy      161 PheAsnG1yAlaG1yCysSerG1yProLeuProIleGlnAlaIleIleTyrlsLeuAspGln 180
Db      567 TTCATATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 626
Qy      181 G1ySerProG1yMetAsnSerThrIleAsnIleHisArgThrSerSerValG1yGlyLeu 200
Db      627 GGAAGCCCTGATGATGATTCACAAATTAATTCATTCAGCACTTCTGCGGAGGACTT 686
Qy      201 CysGlnG1yIleG1yAlaG1yLeuValAlaIleIleTyrlsVal-G1yThrCysSerAs 220
Db      687 TGTGAAGGATGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 746
Qy      220 P1yProArgG1yAspAlaSerThrG1yTrpAsnSerValSerArgIleIleIleG1yG1 240
Db      747 TTACCAAAAGAGAGATGCTTCTACTGATGATGATGATGATGATGATGATGATGATGAA 806
Qy      240 uLeuProLys 243
Db      807 ACTACCCAAA 816

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RESULT 11

AL532456 1098 bp mRNA linear EST 24-MAR-2004
 LOCUS AL532456 Homo sapiens FETAL LIVER Homo sapiens cDNA clone
 DEFINITION CS0DM014YN20 5-PRIME, mRNA sequence.
 ACCESSION AL532456

VERSION AL532456.3 GI:45707373
 EST.
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Li W.B., Gruber C., Jessup J. and Polayes D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT On Feb 13, 2001 this sequence version replaced gi:31070288.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: sequef@genoscope.cns.fr. Web: www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a division of Invitrogen.
 This sequence belongs to sequence cluster 4941.f
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna/8=CS0DM014DG10QPL8=4941.f.

FEATURES

source

1..1098
 location/Qualifiers

/organism="Homo sapiens"
 /mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0DM014YN20"

/tissue_type="FETAL LIVER"

/dev_stage="fetal"

/clone_lib="Homo sapiens FETAL LIVER"

/note="Organ: liver; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

ORIGIN

Alignment Scores:

Pred. No.:	2,46e-109	Length:	1098
Score:	1254.00	Matches:	238
Percent Similarity:	98.35%	Conservative:	0
Best Local Similarity:	98.35%	Mismatches:	4
Query Match:	96.39%	Indels:	1
DB:	1	Gaps:	0

US-10-063-734-122 (1-243) x AL532456 (1-1098)

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Qy      2 ArgProGlnGlyProAlaAlaSerProGlnAArgLeuArgGlyLeuLeuLeuLeu 21
Db      2 CCCCCCGAGGGCCCGCGCTCCCGCAGCGGCTCCGCGCTCTGCTGCTGCTG 61
Qy      22 LeuGlnLeuProAlaProSerSerAlaSerGlnIleProArgGlyLysGlnLysAlaGln 41
Db      62 CTGCAAGTCCCGCGCCGCTCGAGCGCTCTGAGATCCCAAGGGGAAAGGAGGCGAG 121
Qy      42 LeuATGlnArgGlnValValAlaLeuLeuTyraGlnGlyMetCysLeuGlnGlyProAlaGly 61
Db      122 TC-CGCGCAGAGGAGGTGTGAGCTGTATATGAAATGCTTCAAGGGGCGCAGAGGA 180
Qy      62 ValProG1yAArgAspG1ySerProG1yAlaAsnValIleProG1yThrProG1yIlePro 81
Db      181 GTGCTGTGTGAGAGCGGCGCTCGGGGCAATGCAATTCGGGTACCTTGAGATCCCA 240
Qy      82 G1yAArgAspG1yPheLeuGlyG1yLysG1yCysLeuArgGlnLysPheGlnGlnLys 101
Db      241 GGTCCGAGATGATTCAGAGAGAAAGGGGAAATGTCTGAGGAAAGCTTTGAGAGATCC 300
Qy      102 TTPThrProAsnTyrlsGlnCysSerTPSerSerLeuAsnTyrlsIleAspLeuGly 121
Db      301 TGGACACCACTACAGAGAGGTTCATGAGAGTTCATGAAATTAATGAGCATATGATCTGG 360

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QY 122 Lys11ealagluCyThrPheThrIysMetArgSerAsnSerAlaLeuArgValLeuPhe 141
 Db 361 AAAATTGGAGAGTGTACATTTTACAAAGATGCGCTTCAATAGAGCTTAAAGAGTTTGTTC 420
 QY 142 SerG1ysrLeuA1gLeuLysCyArgAsnAlaCySerGlnArgTyrPheThrPhe 161
 Db 421 AGTGCTCAGCTTCGGCTTAAATGCGAATGCAATGCTCTGACGCTGTGATTTTCACTTC 480
 QY 162 AsnG1yAlaGluCySerGlyProLeuProIleGluAlaIleIleTyrLeuAspGlnGly 181
 Db 481 AATGAGCTGATATTTTCAGACCTCTTCCCAATGATATATTTATTTGACCAAGA 540
 QY 182 SerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGluGlyLeuGly 201
 Db 541 AGCCCTAAATGAATTCACAAATTAATATTCATGCACTTCTTGTGGAAGACCTTGT 600
 QY 202 GluG1yIleGlyAlaGlyLeuValAspValAlaIleTyrValGlyThrCySerAspTyr 221
 Db 601 GAAGGATTTGGTGTGATTAAGTGAATGCTATCTGGGTGCGACTTGTTCAGATTAC 660
 QY 222 ProGlyArgAspAlaSerThrGlyTyrAsnSerValSerArgIleIleIleGluGluLeu 241
 Db 661 CCAAAAGAGATGCTTCTACTGATGATGCAATTCAGTTCTTCGCATCATTTATTAAGAACA 720
 QY 242 Prolys 243
 Db 721 CCAAAA 726

RESULT 12
 LOCUS BX387691 986 bp mRNA linear EST 29-APR-2004
 DEFINITION BX387691 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
 clone CS0D1037YD19 5-PRIME, mRNA sequence.

ACCESSION BX387691
 VERSION BX387691
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT On May 8, 2003 this sequence version replaced gi:30461701.

Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with NotI and cloned
 into the NotI and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 4941.f
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdnas2-CS0A1037CB10QPl&c=4941.f.

FEATURES

source
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 location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
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 /issue_type="PLACENTA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with NotI and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:
 Pred. No.:

7.99e-109 Length: 986

Score: 1248.00 Matches: 238
 Percent Similarity: 97.94% Conservative: 0
 Best Local Similarity: 97.94% Mismatches: 5
 Query Match: 95.93% Indels: 1
 DB: 5 Gaps: 0

US-10-063-734-122 (1-243) x BX387691 (1-986)

QY 1 MetArgProGlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeuLeu 20
 Db 93 ATGCCAATCCCAAGAGCGCCCGCCCTCCCGAGCGGCTCCGCGCTCCGCTCCG 152
 QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluIleProIleProIleGlyLysGlnVal 40
 Db 153 CTGCTGACAGCTCCCGCCGCTCCAGCGCTCTGAGATCCCAAGGGAAGCAAGAGGCG 212
 QY 41 GlnLeuArgGlnArgGlyValValAlaLeuTyrArgGlyMetCysLeuGlnGlyProAla 60
 Db 213 CAGTC-CGACAGAGGAGGTGTGAGCTGTATATGATATGCTTACCAAGGCGCAGCA 271
 QY 61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
 Db 272 GGAAGTCTGTGTCAGAGCGGAGCTGGGCGCAATGCAATTCGGGTACCTGGAGATC 331
 QY 81 ProGlyArgAspGlyPheLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100
 Db 332 CAAAGTCCGAGTGAATTCACAAAGAGAAAGGCGGAATGCTCGAGGGAAGCTTTGAGAG 391
 QY 101 SerThrProAlaTyrIleGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 120
 Db 392 TCTGGAACACCACTACCAAGAGTGTATGAGAGTTCATTAATTAATGAGCATAGATCTT 451
 QY 121 GlyIleIleAlaGluCyThrPheThrIysMetArgSerAsnSerAlaLeuArgValLeu 140
 Db 452 GGGAAATTCGGAGGTGTACATTTACAAAGATGCGTTCAATATAGCTCTAAGACTTTG 511
 QY 141 PheSerGlySerLeuArgLeuLysCysArgAsnAlaCysCysGlnArgTyrPheThr 160
 Db 512 TTGAGTGGCTCATTGGCTTAATCAAGAAATGCAATGCTGTACGTTGATTTTCA 571
 QY 161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleTyrLeuAspGln 180
 Db 572 TTCATGAGACTGAATGTCAGGACTCTTCCCATTTGAAGCATATATTATTTGACCA 631
 QY 181 GlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGlyLeu 200
 Db 632 GGAAGCTGAATGAATTCACAAATTAATATTCACACTTCTTGTGGAAGCACTT 691
 QY 201 CysGluGlyIleGlyAlaGlyLeuValAspValAlaIleTyrPValGlyThrCysSerAsp 220
 Db 692 TGTGAAGGAATGCTGCTGATTAAGTGAATGCTATCTGCTGCTGCTGCTGCTGCTGCT 751
 QY 221 TyrProGlyAlaAspAlaSerThrGlyTyrAsnSerValSerArgIleIleIleGluGlu 240
 Db 752 TACCAAAAGAGATGCTTACTGATGATGAAATWCAATTTCTCCCATCATTAATGAAGA 811
 QY 241 LeuProlys 243
 Db 812 CTACCAAAA 820

RESULT 13
 LOCUS CR592899 710 bp mRNA linear HTC 21-JUL-2004
 DEFINITION full-length cDNA clone CS0D1077YB01 of Placenta Cot 25-normalized
 of Homo sapiens (human).
 ACCESSION CR592899
 VERSION CR592899.1 GI:50473706
 KEYWORDS HTC; cDNA.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 710)

QY 19 LeuleuLeuGlnLeuProAlaProSerSerAlaSerGlnLeuProLeuGlyLeuGln 38
 Db 101 CTGCTGCTGTACAGATTGTCGACCCCTCCAGCGCTCTGAGAACCCCAAGCTAGACAA 160
 QY 39 LysAlaGlnLeuArgGlnArgGlnValValAlaLeuLeuTyraGlnGlyMetCysLeuGlnGly 58
 Db 161 AAAGCGCTGATCCGCGAGAGGAGGTGTACCTGTATTAATGAAATGTCTCAAGAA 220
 QY 59 ProAlaGlyValProGlyArgAspGlySerProGlyValAsnValIleProGlyThrPro 78
 Db 221 CCAGCAGAGATTCCCGGTCGTGATGGAGCCCTGGGCGCAAGCGCATTCCTGGACACCT 280
 QY 79 GlyIleProGlyArgAspGlyPheLeuGlyGlyLeuGlyGlyCysLeuArgGlySerPhe 98
 Db 281 GGCATCCAGGTCCGAGATGATTCAAAGGGGAAAGGAGAAATGCTTAAGGAAAGTTT 340
 QY 99 GluGlySerTrpTrpProAsnTrpLeuGlyCysSerTrpSerSerLeuAsnTrpGlyIle 118
 Db 341 GAGAGCTCTGAGACCCCAACTATACAGATGTCGTGAGGTCTGCAACTATGCGCATTA 400
 QY 119 AspLeuGlyLysIleAlaGluCysThrPheThrLysMetArgSerAsnSerAlaLeuArg 138
 Db 401 GATCTTGGGAAATATGGAGAGTGTACATTCACGAAATGGCTCCCAAGTCTCTGCGA 460
 QY 139 ValLeuPheSerGlySerLeuArgLeuLysCysArgAsnAlaCysCysGlnArgTrpTrp 158
 Db 461 GTTCTGTTCAGTGTCTGCTTGGCTCAATGACAGATGCAATGCTGTGACCGCTGTAT 520
 QY 159 PheThrPheAsnGlyAlaGluCysSerGlyProLeuProIleGlnAlaIleIleTrpLeu 178
 Db 521 TTTAACATTAAATGAGATGTAATGTTCAAGACCTCTTCCATCGAAGCATCATCATATCG 580
 QY 179 AspGlnGlySerProGlyLysLeuAsnSerThrIleAsnIleHisArgThrSerSerValGln 198
 Db 581 GACCAAGAGAGCCCTGATTAATCAACTATTAATCAATCAATCAATCAATCAATCAATCA 640
 QY 199 GlyLeuGlyGlnGlyIleGlyAlaGlyLeuValAspValAlaIleLeuValGlyThrCys 218
 Db 641 GGACTCTGAGAGGAGTGTGTGTGATGTGATGTGATGTGATGTGATGTGATGTGATGTG 700
 QY 219 SerAspTrpProGlyGlyAspAlaSerThrGlyTrpAsnSerValSerArgIleIleIle 238
 Db 701 TCAGATTACCCCAAGAGACCTTCTCATGATGATGATTCCTGTCTGATCATCATCAT 760
 QY 239 GluGlyLeuProLys 243
 Db 761 GAAAAAATCAACGAAA 775
 RESULT 15
 AV399086 738 bp DNA linear GSS 15-DEC-2003
 LOCUS Mus musculus CTHRC1 gene, VIRTUAL TRANSCRIPT, partial sequence,
 ACCESSION AV399086
 VERSION AV399086.1 GI:39755075
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 738)
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
 Todd,M.A., Tanenbaum,D.M., Civejlo,D.R., Lu,F., Murphy,B.,
 Adams,M.D. and Cargill,M.
 Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios
 TITLE Science 302 (5652), 1960-1963 (2003)
 JOURNAL 14671302
 PUBMED 2 (bases 1 to 738)
 REFERENCE Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
 Todd,M.A., Tanenbaum,D.M., Civejlo,D.R., Lu,F., Murphy,B.,
 Ferritera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,D.J.,

ADAMS,M.D. and Cargill,M.
 TITLE Direct Submission
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 COMMENT This sequence was made by sequencing genomic exons and ordering
 them based on alignment.
 FEATURES
 source
 1..738
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
 <1..>738
 /gene="CTHRC1"
 /locus_tag="HGM0106"
 ORIGIN
 Alignment Scores:
 Pred. No.: 7.02e-105 Length: 738
 Score: 1205.00 Matches: 229
 Percent Similarity: 94.69% Conservative: 3
 Best Local Similarity: 93.47% Mismatches: 11
 Query Match: 92.62% Indels: 2
 DB: 9 Gaps: 1
 US-10-063-734-122 (1-243) x AV399086 (1-738)
 QY 1 MetArgProGlnGlyProAlaAlaSerProGlnArgLeuArgGly-----LeuleuLeu 18
 Db 1 ATGACACCCCAAGGCG 60
 QY 19 LeuleuLeuGlnLeuProAlaProSerSerAlaSerGlnLeuProLeuGlyLeuGln 38
 Db 61 CTGCTGCTGTACAGATTGTCGACCCCTCCAGCGCTCTGAGAACCCCAAGCTAGACAA 120
 QY 39 LysAlaGlnLeuArgGlnArgGlnValValAlaLeuLeuTyraGlnGlyMetCysLeuGlnGly 58
 Db 121 AAAGCGCTGATCCGCGAGAGGAGGTGTACCTGTATTAATGAAATGTCTCAAGAA 180
 QY 59 ProAlaGlyValProGlyArgAspGlySerProGlyValAsnValIleProGlyThrPro 78
 Db 181 CCAGCAGAGATTCCCGGTCGTGATGGAGCCCTGGGCGCAAGCGCATTCCTGGACACCT 240
 QY 79 GlyIleProGlyArgAspGlyPheLeuGlyGlyLeuGlyGlyCysLeuArgGlySerPhe 98
 Db 241 GGCATCCAGGTCCGAGATGATTCAAAGGCAAAAGGAGAAATGCTTAAGGAAAGCTT 300
 QY 99 GluGlySerTrpTrpProAsnTrpLeuGlyCysSerTrpSerSerLeuAsnTrpGlyIle 118
 Db 301 GAGAGCTCTGAGACCCCAACTATACAGATGTCGTGAGGTCTGCAACTATGCGCATTA 360
 QY 119 AspLeuGlyLysIleAlaGluCysThrPheThrLysMetArgSerAsnSerAlaLeuArg 138
 Db 361 GATCTTGGGAAATATGGAGAGTGTACATTCACGAAATGGCTCCCAAGTCTCTGCGA 420
 QY 139 ValLeuPheSerGlySerLeuArgLeuLysCysArgAsnAlaCysCysGlnArgTrpTrp 158
 Db 421 GTTCTGTTCAGTGTCTGCTTGGCTCAATGACAGATGATGATGATGATGATGATGATG 480
 QY 159 PheThrPheAsnGlyAlaGluCysSerGlyProLeuProIleGlnAlaIleIleTrpLeu 178
 Db 481 TTTAACATTAAATGAGATGTAATGTTCAAGACCTCTTCCATCGAAGCATCATCATCTG 540
 QY 179 AspGlnGlySerProGlyLysLeuAsnSerThrIleAsnIleHisArgThrSerSerValGln 198
 Db 541 GACCAAGAGAGCCCTGAGTAAATTAATCAACTATTAATTAATTAATTAATTAATTAATTA 600
 QY 199 GlyLeuGlyGlnGlyIleGlyAlaGlyLeuValAspValAlaIleLeuValGlyThrCys 218
 Db 601 GGACTCTGAGAGGAGTGTGTGTGATGTGATGTGATGTGATGTGATGTGATGTGATGTG 660
 QY 219 SerAspTrpProGlyGlyAspAlaSerThrGlyTrpAsnSerValSerArgIleIleIle 238
 Db 661 TCAGATTACCCCAAGAGAGCCTTCTCATGATGATGATTCCTGTCTGATCATCATCAT 720

01	239	GlucInleupProLyS	243	
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COMMENT
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@cc.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9216,
Fax: 81-45-503-9216)
Please visit our web site (<http://genome.gsc.riken.jp/>) for further
details.

cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues. First strand cDNA was primed with a primer
[5'-GAGACAGAGAGCGCCGACACTCGATTTTCTTTTTTTTNN 3'], cDNA was
prepared by using trehalose thermo-activated reverse transcriptase
and subsequently enriched for full-length by cap-trapper. Second
strand cDNA was prepared with the primer adapter of sequence [5'
GAGAGGAGAAGAGTCACAGAGCTCATATTATTAATAACCCTCCCC 3']. cDNA was
cleaved with XhoI and SctI. Cloning sites, 5' end; SctI, 3' end;
XhoI. Host: SOLR.

FEATURES
source
Location/Qualifiers
1..1161
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM DB:1110014B07"
/db_xref="taxon:10090"
/clone="1110014B07"
/issue_type="whole body"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
69..806
/dev_stage="18-day embryo"

/note="unnamed protein product; hypothetical Collagen
triple helix repeat containing protein
(InterPro|IPR000087, evidence: InterPro)
putative"
/codon_start=1
/protein_id="BAB22930.1"
/db_xref="GI:12834486"
/translation="MHPQGRAPPRQLILGLVLLILLQSAPISASBNPKYKQALLI
ROREVDLYNMCLOGPAGVRGRSGANGIPTPTPIPRDQGKGKECLRSFE
SWTPNQKCSMSLNYGIDLGKIAETFTMRSSARLVFSGLIRKCRNAACORWYM
FTFGAECGGPLPLEAITIVLDQSPELNTINIHRTSVBGLCEGIGAGLVDAIMWG
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1141..1146
/note="putative"
1161
/note="putative"

polyA_signal
polyA_site

ORIGIN

Alignment Scores:
Pred. No.:
Score: 3.13e-104 Length: 1161
Percent Similarity: 1201.00 Matches: 228
Best local Similarity: 94.69% Conservative: 4
Query Match: 93.06% Mismatch: 11
Indels: 2
DB: 92.31% Gaps: 1

US-10-063-734-122 (1-243) x AK003674 (1-1161)

Gy 1 MeKrArgProGlnGlyProAlaAlaSerProGlnArgLeuArgLy-----LeuLeuLeu 18
Db 69 ATGCACCCCAAGGCCGCGCGCCCCCCCAGCTGCTCGGTCTCTTCCTTGCTG 128
Gy 19 LeuLeuLeuGlnLeuProAlaProSerSerAlaSerGluLeuProLygLylysGln 38
Db 129 CTGCTGCTGCTACAGTTGTCCGCACCGATACAGGCGCTCTGAACAACCCCAAGTAGAACAA 188
Gy 39 LysAlaGlnLeuArgGlnArgGlnValValAspLeuTyTrasnGlyMetCysLeuGlnGly 58
Db 189 CAAACCGCTGATCCCGCAGAGGAGAGGTGTGACCTGTATATGAAATGTCTTCAAGGA 248
Gy 59 ProAlaGlyValProGlyVarGAsnGlySerProGlyValAsnValIleProGlyThrPro 78
Db 249 CCAGCAGAGAGTCCCGGTCGTGAAGGAGCCCTGGGCGCAACGGCATTCCTGGCACACT 308

QY 79 GllYlIeProGlyYArGAspGlyPheLysGlyGluLysGlyGluCysLeuArgGluSerPhe 98
Db 309 GGCAATCCAGGCTCCGGATGATTCAGAAAGGAGAAAGGAGATGCTTAAGGAAAGCTTT 368
QY 99 GluGluSerTrpThrProAntyTyrGlnCysSerTrpSerSerLeuAsnTyrGly118
Db 369 GAGAGATCTCGAGAGCCCAACTATAGAGATGTTCTGAGAGTTCGCTGAACTATGGGATA 428
QY 119 AspleuGlyLysIleAlaGluCysThrPheThrLysMetArgSerAsnSerAlaLeuArg 138
Db 429 GATCTTGGGAAATTTGGAGCTGATTCATTCAGAAAGATGCGCTCAACAGTCTCGCA 488
QY 139 ValLeuPheSerGlySerLeuArgLeuLysCysArgAsnAlaCysCysGlnArgTrpTyr 158
Db 489 GTTCTGTTCAGTGGCTCGCTTCGCTCAAAATGAGAGATGATGCTTCAGCGCTGTAT 548
QY 159 PheThrPheAsnGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleTyrLeu 178
Db 549 TTTACATTATAGAGCTGAATGTTTCAAGACCTCTCCATCGAAGCCATCATCTATCTG 608
QY 179 AspGlnGlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGlu 198
Db 609 GACCAAGAGAGCCCTGATTAATTCATATTTATTTATTCATGCTCTCTCTGAGAA 668
QY 199 GlyLeuGlyGluGlyIleGlyAlaGlyLeuValAspValAlaIleTyrValGlyThrCys 218
Db 669 GGACTGTGTGAAGGATGCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 728
QY 219 SerAspTyrProGlySerAspAlaSerThrGlyTyrAsnSerValSerArgIleIle 238
Db 729 TCGATTATCCCAAGAGAGCGCTTCTTCTGATGAGATTCGCTGCTGCTGATCAT 788
QY 239 GluGluLeuProLys 243
Db 789 GAAAGACTACCGAAA 803

RESULT 17
CA413294/c 716 bp mRNA linear EST 07-NOV-2002
LOCUS UI-H-E20-bap-h-20-0-UI.s1 NCI CGAP Ch1 Homo sapiens cDNA clone
DEFINITION UI-H-E20-bap-h-20-0-UI 3', mRNA sequence.
ACCESSION CA413294
VERSION CA413294.1 GI:24775945
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 716)
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-ri@mail.nih.gov
Tissue Procurement: Dr. Steven Gitelis/ Rush Presbyterian, Dept. of
Orthopedics
cDNA library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
Seq primer: M13 FORWARD
POLYA=Yes
Location/Qualifiers
1..716
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-E20-bap-h-20-0-UI"
/tissue_type="Chondrosarcoma Grade II"
/dev_stage="Adult"

/lab_host="DH10B (Life Technologies)"
/clone_id="NCI CGAP Ch1"
/note="Organ: Left Pelvis; Vector: pUT3-Pac (Pharmacia)
with a modified polylinker. Site 1: EcoR I; Site 2: Not I;
tissue(s): Chondrosarcoma Grade II. The library was
constructed according to Bonaldi, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pUT3-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
TCATCAGCT.
TAG_TISUB=grade-2-chondrosarcoma
TAG_LIB=UI-H-E20
TAG_SEQ=ATCTATATGC"

Alignment Scores:
Pred. No.: 6.1e-104 Length: 716
Score: 1195.00 Matches: 222
Percent Similarity: 99.11% Conservative: 0
Best Local Similarity: 99.11% Mismatches: 2
Query Match: 91.85% Indels: 0
Gaps: 0

US-10-063-734-122 (1-243) x CA413294 (1-716)

QY 20 LeuLeuGluGluLeuProAlaProSerSerAlaSerGluIleProLysGlyLysGlnLys 39
Db 714 CTGCTGCTGACGCTGCCGCGCGCTGAGCGCTTGTGATCCCAAGGAGGAGCAAAAG 655
QY 40 AlaGluLeuArgGlnArgGluValAlaAspLeuTyrAsnGlyMetCysLeuGlnIlePro 59
Db 654 GCGCAGCTCCGGAGAGAGAGGAGGAGTGTGAGCTGTATTAAGATGCTTACAGAGGCA 595
QY 60 AlaGlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGly 79
Db 594 GCAGAGATGCTGCTGTCAGAGCGGAGCCCTGGGCGCAATGAGCATTCGGGTACACTGG 535
QY 80 IleProGlyArgAspGlyPheLysGlyGluLysGlyGluCysLeuArgGluSerPheGlu 99
Db 534 ATCCAGCTCGGATGATTCAGAAAGAGAGAGGAGATGCTTGAAGGAGAGCTTTAG 475
QY 100 GluSerTrpThrProAntyTyrGlnCysSerTrpSerSerLeuAsnTyrGly118Asp 119
Db 474 GAGTCCCTGGACACCAACTACAAAGCAGTGTTCATGAGTTCAATTGATTAATGGATAGT 415
QY 120 LeuGlyLysIleAlaGluCysThrPheThrLysMetArgSerAsnSerAlaLeuArgVal 139
Db 414 CTGGGAAATTCGAGAGTACATTATTAAGAGAGCGCTTCAAAATGAGCTTAAGAGTT 355
QY 140 LeuPheSerGlySerLeuArgLeuLysCysArgAsnAlaCysCysGlnArgTrpTyrPhe 159
Db 354 TTGTTCAAGTGGCTCACTTGGCTTAATGCAAGATGATGCTGACAGTGTATTTTC 295
QY 160 ThrPheAsnGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleTyrLeuAsp 179
Db 294 ACAATTAAATGAGAGTGAATGTCAGAGCTTCCCAATTGAAGCTATTAATTATTTGAC 235
QY 180 GlnGlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGluGly 199
Db 234 CAAGGAGCCCTGAAATGATTCACAAATTAATATTCATGCACTTTCTGAGAGGA 175
QY 200 LeuGlyGluGlyIleGlyAlaGlyLeuValAspValAlaIleTyrValGlyThrCysSer 219
Db 174 CTTTGTGAAGGAAATGCTGCTGATTAATGATGCTGATGCTGATGCTGATGCTGAT 115
QY 220 AspTyrProLysGlyAspAlaSerThrGlyTyrAsnSerValSerArgIleIleGlu 239

Db	114	GATTAACCAAGGANGCTTCACTGAGGAAATTCAGTTCGATCATTTATGA	55
Oy	240	GlutenPolyr 243	
Db	54	GACTACCCAAA 43	
RESULT 18			
LOCUS	AK076498	1168 bp	mRNA linear HTC 03-APR-2004
DEFINITION	Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched library, clone:4833429011 product: hypothetical Collagen triple helix repeat containing protein, full insert sequence.		
ACCESSION	AK076498		
VERSION	AK076498.1	GI:26096845	
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	Carninci, P. and Hayashizaki, Y.		
TITLE	High-efficiency full-length cDNA cloning		
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)		
MEDLINE	99279253		
PUBMED	10349636		
REFERENCE	2		
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.		
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes		
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)		
MEDLINE	20499374		
PUBMED	11042159.		
REFERENCE	3		
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuwa, T., Teshiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, N., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kasahigashi, K., Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.		
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format		
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)		
MEDLINE	20530913		
PUBMED	11076861		
REFERENCE	4		
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.		
TITLE	Functional annotation of a full-length mouse cDNA collection		
JOURNAL	Nature 409, 685-690 (2001)		
MEDLINE	5		
PUBMED	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.		
REFERENCE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs		
AUTHORS	Nature 420, 563-573 (2002)		
TITLE	6 (bases 1 to 1168)		
JOURNAL	Adachi, J., Aizawa, K., Akimura, T., Arikawa, T., Bono, H., Carninci, P., Fukuda, S., Furuta, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hizumoto, K., Hirooka, T., Hirozane, T., Hori, F., Imocani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kachi, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akihira, S., Tanaka, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.		
REFERENCE	Direct Submission		
AUTHORS	Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome		

COMMENT	
<p>EXPLORATION Research Group RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-re@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)</p> <p>cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.</p> <p>Please visit our web site for further details.</p> <p>URL: http://genome.gsc.riken.jp/ URL: http://fantom.gsc.riken.jp/. Location/Qualifiers</p>	
FEATURES	
<p>Source</p> <p>1. 1168</p> <p>/organism="Mus musculus"</p> <p>/mol_type="mRNA"</p> <p>/strain="C57BL/6J"</p> <p>/db_xref="FANTOM DB:4833429011"</p> <p>/db_xref="taxon:10090"</p> <p>/clone="4833429011"</p> <p>/tissue_type="head"</p> <p>/clone_lib="RIKEN full-length enriched mouse cDNA library"</p> <p>/dev_stage="0 day neonate"</p>	
<p>misc_feature</p> <p>/note="hypothetical Collagen triple helix repeat containing protein (InterPro IPR000087, evidence: InterPro)</p>	
<p>polya_signal</p> <p>1148..1153</p> <p>/note="putative"</p>	
<p>polya_site</p> <p>1168</p> <p>/note="putative"</p>	
ALIGNMENT SCORES:	
<p>Pred. No.: 2.58e-102 Length: 1168</p> <p>Score: 1181.00 Matches: 226</p> <p>Percent Similarity: 93.90% Conservative: 5</p> <p>Best local Similarity: 91.87% Mismatches: 12</p> <p>Query Match: 90.78% Indels: 3</p> <p>DB: 3 Gaps: 1</p>	
<p>US-10-063-734-122 (1-243) x AK076498 (1-1168)</p>	
QY	1 MetarproGlnGlyPProAlaAlaSerProGlnArgLeuArgGly-----LeuLeuLeu 18
DB	76 ATGCACCCCCCAAGGCCGCGGCGCCCGCCCGCAGCTGCTCGCTCTTCTTCTGTGCTG 135
QY	19 LeuLeuLeuLeuGlnLeuProAlaProSerSerAlaSerGluLeuProGlyGlyGln 38
DB	136 CTGTGCTGTGACAGTTGTGCCGACCGATCAGCGCTCTGAGAACCCCAAGTGAAGCAA 195
QY	39 LysAlaGlnLeuArgGlnArgGlnValValAspLeuTyrAsnGlyMetCysLeuGlnGly 58
DB	196 AAAGCGCTGATCCGGCAGAGGAGGTGTGACCTGTATATGGAATGTGCTTCAAGGA 255
QY	59 ProAlaGlyValProGlyArgAspGlySerProGlyValAsnValIleProGlyThrPro 78
DB	256 CCGACGAGAGTCCCGGTCGTGATGGGAGCGCTGGGSCCAACGGCATTTCTGGGACACCT 315
QY	79 GlyIleProGlyArgAspGlyPheLeuGlyGlyGlyGluCysLeuArgGluSerPhe 98
DB	316 GGCATCCAGATGGGATGATTCAAAGGGGAAAAAGGAGAGATCTTAAGGAAAAGCTTT 375
QY	99 GluGluSerThrProAsnTyrLysGlnCysSerTrpSerSerLeuAsnTyrGlyIle 118
DB	376 GAGGAGTCTCGACCCCAACTAATAACAGATGTTCTGTGAGTTCTGGAACATAAGGCATA 435
QY	119 AspLeuGlyLysIleAlaGluCysThrPheThrLysMetArgSerAsnSerAlaLeuArg 138
DB	436 GATTTGGGAAAATTGGAGATGTACATTCACGAAGATGGCGCTCAACAAATGCTTCGCA 495

	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
Qy	139	ValLeuPheSerGlySerLeuAlaLeuLeuGlyGlyArgAsnLysAcGlyCysGlnArgTyr	AL553798	709 bp	mrna	linear	EST 30-MAR-2004
Db	496	GTTCTGTTCAGTGGCTCGCTTCGGCTCAATGACGAAATGCATGCTGTACCGCTGGTAT	AL553798	clOne CS0D107YB01 5-PRIME, mRNA sequence.			Homio sapiens CDNA
Qy	159	PheThrPheAsnGlyIaGluCysSerGlyPro-LeuProIleGluAlaIleIleTyrIle	AL553798	EST.			Homio sapiens (human)
Db	556	TTTACATTATATGAGCTGAAATGTCAGACCTTCCTCCATGGAAGCCATCATCTATCT	AL553798	EST.			Homio sapiens
Qy	178	UaAPGInGlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValG	AL553798	EST.			Homio sapiens
Db	616	GGACCAAGGAAGCCCTGAGTTAAATCACTATTAATTCATGCACTTCCTGTGGA	AL553798	EST.			Homio sapiens
Qy	198	uGlyLeuCysGluGlyIleGlyAlaGlyLeuValaIaPValaIaIleTyrValGlyThrCy	AL553798	EST.			Homio sapiens
Db	676	AGGACCTCTGGAAGGATAGTCTGGATGTGATATGTGGCATCTGGGTGGGCACTTG	AL553798	EST.			Homio sapiens
Qy	218	sSerAerPyrProIyGlyAspAlaSerThrGlyTTPaenSerValSerArgIleIleI	AL553798	EST.			Homio sapiens
Db	736	TTTCAGTTTACCCCAAGAGACCGCTTCATCTGATGAATTCGTTCTTCGATCATCAT	AL553798	EST.			Homio sapiens
Qy	238	eGluGluLeuProIyS 243	AL553798	EST.			Homio sapiens
Db	796	TGAAGACTACCGAA 811	AL553798	EST.			Homio sapiens
RESULT 19							
AL553798							
LOCUS							
DEFINITION							
ACCESSION							
VERSION							
KEYWORDS							
SOURCE							
ORGANISM							
REFERENCE							
AUTHORS							
TITLE							
JOURNAL							
COMMENT							

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FEATURES
  source
    for more information about this cluster, see
    http://www.genoscope.cns.fr/cdna?c=CS0D1077CA01Q1P1&c=4941.f
    Location/Qualifiers
    1..709

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI077YB01"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_id="Homo sapiens PLACENTA COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

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Pred. No.:	6,14e-102
Score:	1174.00
Percent Similarity:	97.38
Best Local Similarity:	97.38
Query Match:	90.24
	Indels: 1
	Mismatches: 6
	Conservative: 0
	Matches: 223
	Length: 709

DB:	1	Gaps:	0
US-10-063-734-122 (1-243)	x	AL553798 (1-709)	

OY		15	G VleuuenuenuenuenuenuenuenuenLnuProlAProSerSeralAsergluilePro	34
Dd		6	GGATTCCTGCTGCCTCGCTGCAGCAGCCGCCGCCCTCCAGGCGCTCTGACGATCCCC	65
OY		35	LysGIYLysGIILySaIagInuEuArfgInARgIUvaIVaIAspLeuTYRAnGIYnec	54
Dd		66	AAGGGGAAGCAAAAGCGCGCA-CTCCGGCAGAAGAGAGCTGTGTGACTTATAATGAATG	122
OY		55	CyleuGIuGLlyProAlaGIyValProGIYAraApGIYserProGIYAlaAsnValIle	74
Dd		125	TGCTTAACAAGGCGCACAGAGTGCTGTTCAGACGGAGACCCTGGGGCCAATGCAATT	189
OY		75	ProGIYThProGIYIleProGIYARAapGIYPhelysGIYgluLYsglucInCyaleu	94
Dd		185	CCGGGTACACCTGGGATGCCAGTGGGATGATTCANAGAGAAAAGGGGAATGTCTG	244
OY		95	ArgGIUsErPheluglUlsErTrThrProAntYrLySGlnCYsErTPserSerLeu	114
Dd		245	AAGGAAGCTTTGAGAGAGCTCCGACACCCAACTAACAGCAGTGTTCATGAGATTCA TTG	304
OY		115	AsnTYrgLIleaspLeuGIYlysIIleaglucYsrThPhemTrlysmcArgrSerAsn	134
Dd		305	AATTAATGGCATMGATCTTGAGAAATTCGAGAGGTACATTTACAAAGATGCGTCAAT	364
OY		135	SerAlalaEuhgValleuPheserGIYSerleuArgleuLYsCYsArqAnaIacyCYs	154
Dd		365	AGTGCTCTRAAGAGTTTTTGTTCAGTGGCTCACCTTGGCTCAAATSCAANAATGCA TGTGTGT	424
OY		155	GlnArGIrPIYrPhethePhAsnGIYAlaagInuCYsSerGIYProleuProIIegluAla	174
Dd		425	CAGCGTGGTATTCACATTCAGATGAGACTGAAATGTCAGAGACTCTCTCCATTTGAAGCT	484
OY		175	IlelleIYrleuAspGlnGIYSerProGIUnetAmSerThrIleasnIIeHISarGTThr	194
Dd		485	ATAAATTTATTTGGACCAAGAGAGCCCTGAAATGATTCACAATTAATATATTCACACT	544
OY		195	SerSerValGIuGLyLeuCYsGlUGlYIIleGIYAlaaglYeuValAspValAlaIleTP	214
Dd		545	TCTTCTGTGGAAGACATTTGTGAAGAGAAATGTGTGTGATTAATGATGTGTCTA CTGG	604
OY		215	ValGIYThrcYssEraPYrProLYsgIYAspAlaserThrGIYTrpAsnSerValser	234
Dd		605	GTTGTGATCTGTTCAAGATTACCCAAAGAGATGCTTCACTGAGTAGGAATMTTTC TA	664
OY		235	ArgIleIleIleGIuGLyLeuProLYs	243
Dd		665	CGCATTCATTATTAAGAACTACCAAA	691

RESULT 20
LOCUS BX386416
DEFINITION BX386416 Homo sapiens PLACENTA COR 25-NORMALIZED Homo sapiens CDNA
ACCSSION clone GCSDD1077YB01 5-PRIME, mRNA sequence.
VERSION BX386416
KEYWORDS BX386416.2 GI:46627527
SOURCE EST.
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (base 1 to 707)
L1, W.B., Gruber, C., Jesse, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 8, 2003 this sequence version replaced gi:30457424.
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

QY	60	AlGLIYAlProGIYAAGAspGIYseProGIYAlAsnValIIleProGIYThProGIY	79
Db	181	GCAGAGATTCCTCCGTCGTGATGGAGGCCCTGGGGCCCAACGGCAATTCCTGGACACCTGGC	240
QY	80	IIleProGIYAAGAspGIYPhelysGIYGlulysGIYCySleuAArgIuSerPheGIu	99
Db	241	ATCCAGAGTCGGAGTGGATTCAAAAGGGGAAAGGGAGAAATCTTAAGGAAAGCTTTGAG	300
QY	100	GIuSerTTrpThrProAsnIYLYsGIuCySerTTrpSerSerIeuAsnIYGIYIleAsp	119
Db	301	GAACTCCTGGACCCCAACTATAAGCAGCTGTTGCGAGATTCGCTGAACTAATGCGATGAT	360
QY	120	LeuGIYLYsIIleIaGIuCySthPrpThIYsHeIArgSerAsnSerAlaIeuArgVal	139
Db	361	CTTGGGAAATTCGAGGTAACTATCAGAAAGATGGCTCCCAACATGCTCTGGCAGATT	420
QY	140	LeuPheSerGIYSerIeuAArgIeulysCySArgAsnAlaCySArgIuAArgTTrpIYrPhe	159
Db	421	CTGTTAGTGGCTCGCTCGCTCCCAATGACGAATCAAGCTGTCAAGCCCTGTTATTTT	480
QY	160	ThrPheAsnGIYAlaGIuCySerGIYProIeuProIIleGIuAlaIIleIYrIleuAsp	179
Db	481	ACAATTTAAACGAGCTGAATGTTCAGAGACCTCTTCCCATGCAAGCANCATCATCTCGAC	540
QY	180	GIuGIYseProGIuIuIeuAsnSerThrIIeAsnIIleHISArgThrSerSerValGIuGIY	199
Db	541	CNAGGAAGCCCTGAGTTAAATTCATACTATTAAATTCATCGTACTCTCTT-----GGA	594
QY	200	LeuCySGluGIYIIleGIYAlaGIYLeuValAspValAlaIIleHrValGIYThrCySser	219
Db	595	CTCTGGAAGGAGATTCGTGCTGATTTGGTNGATGTGCAATCTGGGCTGGACACTTATCA	654
QY	220	AspIYrProIySGIYAspAlaSerThr-GIYTrpAsnSerValSerArgIIleIIleGI	239
Db	655	GATTACCCCAAGAGAGACGCTTCTACTTGGATGGAATTCGGTGTCTCGCATATCATTTGA	714
QY	239	uGIuIeuProIys 243	
Db	715	AGAACTACCGAAA 727	

RESULT 22	BX386415/c	670 bp	mRNA	linear	EST 27-APR-2001
LOCUS	BX386415				
DEFINITION	BX386415 Homo sapiens PLACENTA COR 25-NORMALIZED Homo sapiens cDNA clone CS001077YB01 3-PRIME, mRNA sequence.				
ACCESSION	BX386415				
VERSION	BX386415.2	GI:46622720			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1. (bases 1 to 670)				
AUTHORS	Li, W.B., Gruber, C., Jessee, J., and Polayes, D.				
TITLE	Full-length cDNA libraries and normalization				
JOURNAL	Unpublished (2001)				
COMMENT	On May 8, 2003 this sequence version replaced gi:10455415				

REACTURES

Contact: Genoscope
Genoscope - Centre National de Séquençage
BP 191 91006 Evry cedex - France
Email: sege@genoscope.cns.fr Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dt) primer. Five primers
end enriched double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
4941.f

For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?s=CSIA1020ZB01NP1&c=4941.f>.
10873000/D_11f.f

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FEATURES
source
location/Qualifiers
1..670
/organism="Homo sapiens"

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/mol_type="mrna"
/db_xref="taxon:9606"
/ci_name="CS0D1077YB01"
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo (GT)
primer. Five prime end enriched, double-strand, cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. library was normalized."

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Alignment Scores:

Freu, MO.:	1.58e-98	Length:	2110
Score:	1378.00	Matches:	1
Percent Similarity:	98.15%	Conservative:	1
Best Local Similarity:	97.69%	Mismatches:	4
Query Match:	87.47%	Indels:	0
DB:	5	Gaps:	0

US-10-063-734-122 (1-243) X BX386415 (1-670)

15 GYLVLEULEULEULEULEULEUGLNUFLQALAPROSETERALASERGLUILEPRO 34
 27 ...
 Db 668 GGGARTCCITGCTCCTGCTGCACTGCTCCGCGCCGTCGAGCGCCCTCTGAGATCCCC 60

QY LysGlyLysGlnLysIleuArgIleArgIleValIleAspLeuTyrAsnGlyMet 54
 Db MGGGGAGCGAAMGGCGCACTCCGGCAGAGGAGGCTGTGCACTGTATAGGATG 54
 608

QY 55 CysLeuGlnGlyProAlaGlyValProGlyArgAspGlySerProGlyValAlaSerValIle 74
Db 548 TGCTCACAAAGGGCCAGCAGAGTGCTGTGTGTCAGACGGAGACCTGGGGCCAAATGCAT 48

QY 75 ProGlyThrProGlyVileProGlyArgAspGlyPheIysGlyGluIysGlyGluCysIeu 94
Db 488 CCGGGACACCTGGGATCCAGGTGGGATGTATTCTAAAGAGAGAAAGCCCGGATTTCTTC 422

95 ArgGlusErPheglUglusErTIpThrProasnTyLysGlnCysSerTrpSerSerIleu 11

[illegible]

QY 135 SerAlaIleuArgValIleuPheSerGlySerIleuArgIleuLysCysArgAsnAlaCysGly 154

155 GlnArgTrpTyrPheThrPheAsnGlyAlaGluCysSerGlyProLeuProIleGluAla 174

175 IleIeIeYrLeuapGInGlySerProGIuMetasnsrThrIleasnIleHisArgThr 194

195 SerSerValGluGlyLeuCysGluGlyIleGlyAlaGlyLeuValAspValAlaIleTrp 214

ValGlyThrCysSerAspTyrProLysGluAspAlaSerThrGlyTyr 230
|||||
|||||

68 GTGGTACTCTGTGAGATTACCCAAAGAGAGANGCTTCTACTGATGG 21

LOCUS	671 bp	mRNA	linear	EST 23-SEP-200
BU622465				
UI-H-FG1-bgk-c-06-0-UI.s1	NCI	CGAP	Fgi Homo sapiens	cdna clone
UI-H-FG1-bgk-c-06-0-UI 3'				mRNA sequence.

accession BU624465
 version BU624465.1
 keywords EST.

SOURCE Homo sapiens (human)

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 671)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapdb-r@mail.nih.gov
Tissue Procurement: James Martin
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, Bento-Soares@uiowa.edu
The following repetitive elements were found in this cDNA sequence: 1-28, >AT rich#Low_complexity
Seq primer: M13 FORWARD
POLYA=yes

FEATURES

Source

Location/Qualifiers

1..671

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="UI-H-FGI-bqk-c-06-0-UI"

/tissue_type="Cell lines"

/dev_stage="Adult"

/lab_host="NCI CGAP FGI"

/note="Organ: Enchondroma; Vector: p773-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP FGI is a normalized cDNA library obtained from a pool of mRNA from 2 cell lines from Enchondroma tissues. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into p773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CGTCACCTC. The cell lines were provided by Dr. James Martin from the University of Iowa.
TAG_TISSUE=Enchondroma cell line (M1x of EN1 and EN2)
TAG_LIB=UI-H-FGI
TAG_SEQ=CGTCACCTC"

ORIGIN

Alignment Scores:

Pred. No.: 1.98e-98 Length: 671

Score: 1137.00 Matches: 210

Percent Similarity: 99.064 Conservative: 0

Best Local Similarity: 99.064 Mismatches: 2

Query Match: 87.398 Indels: 0

DB: 5 Gaps: 0

US-10-063-734-122 (1-243) x BU624465 (1-671)

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DB 671 G|A|A|T|C|C|C|A|A|G|G|A|A|A|G|G|C|G|C|C|G|C|A|A|G|G|A|G|G|T|G|A|C|C|T|G|A|T 612

QY 52 A|e|n|g|l|y|e|t|C|y|e|l|e|u|g|l|n|g|l|y|P|r|o|a|g|l|y|a|l|P|r|o|g|l|y|A|r|g|a|s|p|l|y|S|e|r|P|r|o|g|l|y|A|l 71

DB 611 A|A|T|G|A|A|T|G|C|T|T|A|C|A|G|G|C|C|A|G|A|G|A|G|T|C|C|G|T|C|G|A|G|A|C|G|G|A|G|C|C|T|G|G|G|C 552

QY 72 A|e|n|l|l|e|P|r|o|g|l|y|T|h|r|P|r|o|g|l|y|l|e|P|r|o|g|l|y|A|r|g|a|s|p|l|y|P|h|e|l|y|s|g|l|y|l|u|y|s|g|l|y 91

DB 551 A|A|T|G|C|A|T|T|C|G|G|G|T|C|A|C|C|T|G|G|A|T|C|C|A|G|G|T|C|G|G|A|T|G|A|T|T|C|A|A|G|A|G|A|A|G|G|G 492

QY 92 G|U|C|y|L|e|A|r|g|u|S|e|r|P|h|e|G|l|u|S|e|r|T|P|r|o|A|s|T|y|l|y|e|G|l|n|C|y|S|e|r|T|P 111

DB 491 G|A|A|T|C|T|G|A|G|G|A|A|G|C|T|T|G|A|G|A|G|T|C|T|G|A|C|A|C|C|A|C|T|A|C|A|G|A|G|T|C|T|A|G 432

QY 112 S|e|r|S|e|r|L|e|u|e|r|T|y|l|e|a|s|p|l|e|u|g|l|y|s|l|e|a|l|u|C|y|e|T|h|P|h|e|T|h|y|S|e|t 131

DB 491 A|G|T|C|A|T|G|A|A|T|T|A|T|G|G|A|T|G|G|A|A|A|T|T|G|G|G|A|G|T|T|A|C|A|A|A|G|A|G 372

QY 132 A|r|g|S|e|r|A|n|S|e|r|A|l|e|u|a|r|g|V|a|l|e|u|P|h|e|S|e|r|g|l|y|S|e|r|L|e|u|e|r|y|e|C|y|A|r|g|A|n 151

DB 371 C|G|T|T|A|A|A|T|G|C|T|T|A|G|A|G|T|T|G|T|C|A|G|T|G|C|T|C|A|C|T|G|G|C|T|A|A|A|T|G|C|A|A|A|T 312

QY 152 A|A|C|y|S|G|l|n|A|r|T|y|P|r|P|h|e|r|P|h|e|a|n|g|l|y|A|l|u|C|y|S|e|r|g|l|P|r|o|l|e|u|P|r 171

DB 311 G|C|A|T|C|T|G|C|A|G|C|G|T|T|G|G|A|T|T|C|A|T|T|C|A|T|G|A|G|C|G|A|T|T|C|A|G|A|C|T|T|C|C 252

QY 172 I|l|e|g|u|a|l|l|e|l|e|T|y|l|e|u|S|p|l|n|g|l|y|S|e|r|P|r|o|l|e|u|e|r|S|e|r|T|h|l|e|a|n|l|e 191

DB 251 A|T|T|G|A|G|C|T|A|T|A|T|T|A|T|T|G|G|A|C|C|A|G|A|G|C|C|T|G|A|A|T|G|A|T|T|C|A|A|C|A|T|T|A|T|T 192

QY 192 H|l|e|r|g|T|S|e|r|S|e|r|V|a|l|G|l|u|l|y|e|u|C|y|S|g|l|y|l|e|g|l|y|A|l|u|e|V|a|l|e|P|V|a| 211

DB 191 C|A|T|G|C|A|C|T|T|C|T|G|G|A|G|A|G|A|C|T|T|G|T|G|A|G|A|A|T|T|G|T|G|A|T|T|A|G|T|G|A|T|T 132

QY 212 A|A|l|e|T|P|V|a|l|G|l|y|T|h|C|y|S|e|r|A|s|P|T|y|P|o|l|y|S|G|l|A|s|P|A|S|e|r|T|h|g|l|T|P|A|S|n 231

DB 131 G|C|T|A|C|T|G|G|G|T|T|G|G|A|C|T|T|G|T|C|A|T|T|C|C|A|A|A|G|A|G|A|G|C|T|T|C|T|A|C|T|G|A|T|G|A|T 72

QY 232 S|e|r|V|a|l|S|e|r|A|l|l|e|l|e|l|e|G|l|u|l|e|u|P|r|o|l|y|S 243

DB 71 T|C|A|G|T|T|C|G|C|A|T|C|A|T|T|A|T|T|G|A|A|C|A|C|A|A|A 36

RESULT 24

AL553771/C 676 bp mRNA linear EST 30-MAR-2004

LOCUS AL553771 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA

DEFINITION clone CS001077YB01 3-PRIME, mRNA sequence.

ACCESSION AL553771

VERSION AL553771.3 GI:45858536

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

1 (bases 1 to 676)

Li, W.B., Gruber, C., Jesse, J., and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On Feb 15, 2001 this sequence version replaced gi:31275585.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: sequenc@genoscope.cns.fr, Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 4941.f

For more information about this cluster, see <http://www.genoscope.cns.fr/cdna?e=CS001077CA01NP1&c=4941.f>.

FEATURES

source

Location/Qualifiers

1..676

/organism="Homo sapiens"

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/clone="CS001077YB01"

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/note="1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

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 Db 723 TTGTGAAGAGATTGGCTGGATTTAGATTCAGATTCGGGTTGGCACTGTT 782
 QY 219 exaspyrprolysglyaspaasethrglytrpanservalserarg----- 235
 Db 783 TCCAAATACCCCAAGAGAGATGCTTCTTACTGAGAGGAATTCAGTTTCTCGCA 842
 QY 236 --llellellegluleuproly 243
 Db 843 TCATTATTGGAGAACTACCCAAA 868

RESULT 26
 BU624261/c 654 bp mRNA linear EST 23-SEP-2002
 LOCUS UI-H-FGI-bgj-j-13-0-UI.61 NCI CGAP FGI Homo sapiens cDNA clone
 DEFINITION UI-H-FGI-bgj-j-13-0-UI 3', mRNA sequence.
 ACCESSION BU624261
 VERSION BU624261.1 GI:23290476
 KEYWORDS EST.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 654)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov

JOURNAL
 COMMENT
 Tissue Procurement: James Martin
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be obtained
 from Dr. M. Bento Soares, bento-soares@uiowa.edu
 The following repetitive elements were found in this cDNA
 sequence: 1-28, >AT-richLow_complexity
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES
 source Location/Qualifiers

1..654
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-H-FGI-bgj-j-13-0-UI"
 /issue_type="Cell lines"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="NCI CGAP FGI"
 /note="Organ: Enchondroma; Vector: pT73-Pac (Pharmacia)
 with a modified polylinker; Site 1: Ecor I; Site 2: Not I;
 NCI CGAP FGI is a normalized cDNA library obtained from a
 pool of mRNA from 2 cell lines from Enchondroma tissues.
 The library was constructed according to Bonaldo, Lennon
 and Soares, Genome Research, 6:791-806, 1996. First strand
 cDNA synthesis was primed with an oligo-dT primer
 containing a Not I site. Double stranded cDNA was ligated
 to an Ecor I adaptor, digested with Not I, and cloned
 directionally into pT73-Pac vector. The oligonucleotide
 used to prime the synthesis of first-strand cDNA contains
 a library tag sequence that is located between the Not I
 site and the (dT)18 tail. The sequence tag for this
 library is CGTCATC.
 James Martin from the University of Iowa.
 TAG TISSUE=Enchondroma cell line (Mix of EN1 and EN2)
 TAG_LIB=UI-H-FGI
 TAG_SEQ=CGTCATC"

ORIGIN

Alignment Scores:

Pred. No.: 4,7e-96
 Score: 1112.00
 Percent Similarity: 99.51%
 Best Local Similarity: 99.51%
 Query Match: 85.47%
 DB: 5
 Gaps: 0

US-10-063-734-122 (1-243) x BU624261 (1-654)

QY 38 GlnlysalaglnleuargglnarggluvalaapleuTyraBnglywecysleugln 57
 Db 653 CAAAGGCGCAGACTCCGCGAGAGAGGTGGAGCCTGTATAATGCAATGCTTACAA 594
 QY 58 GTPProAlaGlyValProGlyVArgAspGlySerProGlyAlaAsnValIleProGlyThr 77
 Db 593 GGCCAGAGAGAGTGCCTGGTGCAGACGGAGCCCTGGGGCCAAATGGCAATTCGGGTACA 534
 QY 78 ProGlyIleProGlyVArgAspGlyPheGlyGlyGlyGlyGlyGlyGlyGlyGly 97
 Db 533 CTTGGATCCAGGTCGGATGGAATTCAGAGAGAGAGAGAGAGAGATGCTGAGGAGAAC 474
 QY 98 PheGlnGlySerTrpThrProAsnTrpGlyGlyGlyGlyGlyGlyGlyGlyGly 117
 Db 473 TTGAGAGAGTCTTGAGACCAACTACAGAGGTTCATGAGTTCAATATATGCG 414
 QY 118 IleAspLeuGlyValIleAlaGlyGlyThrPheThrIleMetArgSerAsnSerAlaLeu 137
 Db 413 ATAGATCTTGGAGAAATTCGGAGGTATCATTTACAAAGATCGTTCAATATGTCCTCA 354
 QY 138 ArgValIleuPheSerGlySerleuArgleuGlyGlyGlyGlyGlyGlyGlyGlyGly 157
 Db 353 AGAGTTTGTTCAGTGGCTCACTTCGGCTAAATGCAAGATCATGCTTCAGCCTTG 294
 QY 158 TyrPheThrPheAsnGlyValaGlnGlyGlyGlyGlyGlyGlyGlyGlyGly 177
 Db 293 TATTCACATTCATAGAGAGCTGAATGTTGAGAGACCTTCCTCATGAGCTAATTTAT 234
 QY 178 LeuAspGlnGlySerProGlyMetAsnSerThrIleAsnIleHisArgThrSerSerVal 197
 Db 233 TTGGACCAAGAGAGCCCTGAATGAAATTCAGAAATTAATTCATCGCACTTCTCTG 174
 QY 198 GlnGlyLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 217
 Db 173 GAGAGACTTGTGAAGAGATTCGTCTGCTGATTCGATTCGATTCGATTCGATTC 114
 QY 218 CysSerAspTyrProlysglyaspaasethrglytrpanservalserargylelle 237
 Db 113 TTTTCAATTCACCAAGAGAGATGCTTCTACTGATGGAATTCAGTTTCTCGCATCATT 54
 QY 238 lleGlnGluLeuProly 243
 Db 53 ATTTGAAGAACTACCAAAA 36

RESULT 27
 BM915926 1037 bp mRNA linear EST 12-MAR-2002
 LOCUS AGENCOURT_6639781 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5482196
 DEFINITION 5', mRNA sequence.
 ACCESSION BM915926
 VERSION BM915926.1 GI:19366305
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 1037)
 NIH-MGC <http://mhc.ncbi.nlm.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 JOURNAL
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: DCTD/DTP

CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
 Plate: LUCM2007 row: n column: 21
 High quality sequence stop: 482.

FEATURES

1. 1037
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5482196"
 /issue_type="amelanotic melanoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_id="NIH_MGC_41"
 /note="Organ: skin; Vector: pOT7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGACGAG(G). Library constructed by Ling Hong in the
 laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 2,95e-95 Length: 1037
 Score: 1106.50 Matches: 219
 Percent Similarity: 94.44% Conservative: 2
 Best Local Similarity: 93.59% Mismatches: 8
 Query Match: 85.05% Indels: 5
 DB: 4 Gaps: 1

US-10-063-734-122 (1-243) x BW915926 (1-1037)

QY 1 MetATGProGlnG1ProAlaIaSerProGlnArgLeuArgGlyLeuLeuLeuLeu 20
 Db 86 ATGCCAGCCCAAGGCCCCCGCCCTCCCGCAGCGGCTCCGCGCTCTGCTGCTCCTG 145
 QY 21 LeuLeuGlnLeuProAlaIaProSerSerAlaSerGluLeuProGlyLYsGlnLYsAla 40
 Db 146 CTGCTGCAGCTGCCGCGCGCTCGAGCGCTCTGAGATCCCAAGGAGCAAGAGCG 205
 QY 41 GlnLeuArgGlnArgGluValValAspLeuLYsAsnGlyMetCysLeuGlnGlyProAla 60
 Db 206 CAGCTCCGCGAGGAGGAGGTGGTGAACCTGTAATGGAATGCTTACAGAGGCAACA 265
 QY 61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
 Db 266 GGAAGTCTGGTGCAGAGAGGAGCCCTGGGCGCAATGCGATTCGAGTACACCTGGAGTC 325
 QY 81 ProGlyArgAspGlyPheLYsGlyGlyLYsGlyGlyCysLeuArgGlySerPheGluGlu 100
 Db 326 CCAAGTCCGAGATGATCAAGAGAGAGAGGAGGAAATGCTGAGAGGAAAGCTTGAAGAG 385
 QY 101 SerThrProAsnLYsGlyGlySerThrPheSerSerLeuAsnLYsGlyIleAspLeu 120
 Db 386 TCCGAGACACCACTACAGACAGTTCATGAGATTGATGAATTAAGGATGATGATCTT 445
 QY 121 GlyLYsIleAlaGluCysThrPheThrLYsMetArgSerAsnSerAlaLeuArgValLeu 140
 Db 446 GGGAAATTCGGGAGTGAATTAACAAGATGGCTTAATATGCTTAAAGATTTC 505
 QY 141 PheSerGlySerLeuArgLeuLYsCysArgAsnAlaCysCysGlnArgTyrPheThr 160
 Db 506 TTCAGTGCCTACTTCGCTTAAATGCAACAATCAGTCTGTCAGCTTGGTATTTCACG 565
 QY 161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleLYsThrLeuAsnGln 180
 Db 566 TTCATAGAGACTGAATGTCAGACCTCTTCCCTTAAGCTTAATTAATTGAGACCA 625

QY 181 GlySerPro-GluMetAsnSerThrIleAsnIleHisArg-ThrSerValGluLYL 200
 Db 626 CGAAGCCCTCGAAGAAATGAAATTCACATATGATTCATCCGAGACTTCTCTGTGGAAGAC 685
 QY 200 euCYsGlnGlyIleGlyValGlyLeuValAspValAlaIleTyrVal--GlyThrCys 219
 Db 686 TTTCGAGAGAAATTCGCTGCTGATTAAGTGTGTATTCGAGGCTTGGGACTTGTTC 745
 QY 219 rAspTyrProLYsGlyAspAlaSerThrGlyTyr 230
 Db 746 ACATATCCCAAGAGAAATGCTTCCACC---TGG 776

RESULT 28
 LOCUS BQ425266
 DEFINITION AGENCOURT_7912803 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6150166
 5', mRNA sequence.
 ACCESSION BQ425266
 VERSION BQ425266
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 851)
 AUTHORS NIH-MGC <http://mgc.ncl.nih.gov/>,
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strauberg, Ph.D.
 Email: rgs@rs-riemail.nih.gov
 Tissue Procurement: ATCC/DC/DTP
 CDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
 Plate: LLM13484 row: f column: 23
 High quality sequence stop: 670.
 Location/Qualifiers

FEATURES

source

1. 851
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6150166"
 /issue_type="amelanotic melanoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_id="NIH_MGC_72"
 /note="Organ: skin; Vector: PCMV-SPORE6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally. Primer: oligo dT.
 Average insert size 2 kb. Library constructed by Life
 Technologies."

ORIGIN

Alignment Scores:

Pred. No.: 3.14e-95 Length: 851
 Score: 1105.00 Matches: 216
 Percent Similarity: 95.61% Conservative: 2
 Best Local Similarity: 94.74% Mismatches: 6
 Query Match: 84.93% Indels: 4
 DB: 5 Gaps: 2

US-10-063-734-122 (1-243) x BQ425266 (1-851)

QY 1 MetATGProGlnG1ProAlaIaSerProGlnArgLeuArgGlyLeuLeuLeuLeu 20
 Db 168 ATGCCAGCCCAAGGCCCCCGCCCTCCCGCAGCGGCTCCGCGCTCTGCTGCTCCTG 227
 QY 21 LeuLeuGlnLeuProAlaIaProSerSerAlaSerGluLeuProGlyLYsGlnLYsAla 40
 Db 228 CTGCTGCAGCTGCCGCGCGCTCGAGCGCTCTGAGATCCCAAGGAGGAGAGCGG 287
 QY 41 GlnLeuArgGlnArgGluValValAspLeuLYsAsnGlyMetCysLeuGlnGlyProAla 60


```
Db 288 CAGCTCCGACAGGGAGGTGGACCTGTATTAATGATGCTTACAGGCGCCAGCA 347
Qy 61 G1yValProG1yAArgApG1ySerProG1yAlaAenVal11leProG1yThProG1yIle 80
Db 348 GGAAGTCCCTGGTCTGACACCGGAGCCCTGGGGCCAAATGAGATTCCGGGTACACCTGGGATC 407
Qy 81 ProG1yAArgApG1yPhelYsg1yG1yValYsg1yCylLeuAArg1yUserPheG1yUgu1y 100
Db 408 CCAAGTCGGGATGATTCATCAAGAGAAAGGGGAAATGCTGAGGGAAAGCTTTGAGGAG 467
Qy 101 SerTTPThProAenTYrYsg1yCysSerTTPSerSerLeuAenTYrG1yIleApleu 120
Db 468 TCCTGGACACCCACACACAGAGAGTGTTCATGAGATTGATTAATGACATGATCTT 527
Qy 121 G1yYVal1leA1yG1yCysThrPheThYrYMetAArgSerAenSerA1eAenYVal1leu 140
Db 528 GGGAAATATGCGAGATGATTCATTAACAAAGATGCGTTCAAAATAGTCTCTAAAGATTG 587
Qy 141 PheSerG1ySerLeuAArgLeuYsCyAArgAenAlaCyCySg1yAArgTTPYrPheThr 160
Db 588 TTCAGTGGCTCACTTCGCTAAATCAAGAAATGATGCTGTCAGCGTGGATTTGACCA 647
Qy 161 PheAenG1yAlaG1yCysSerG1yProLeuPro11eG1yAla1le1leTYrLeuAepG1n 180
Db 648 TTCATGAGAGCTGAATGTTCAAGACCTCTCCCATTTGAAGCTATATTATTGACCA 707
Qy 181 G1ySerProG1yMeAenSerThYr1leAen11leH1AArgThSerSerValG1yUgu1yLeu 200
Db 708 GGAAGCCCTGGAATGATTCACAAATTAATTCATCGACCTCTCTGGAAGACAT 767
Qy 201 CySg1y-G1y1leG1yAlaG1y-LeuValAAspVala1a---11eTTPValG1yThCyS 219
Db 768 TGTGAAGAAATTTGCTGCGAATTATGAGATGTTGCTATCTGGGGGAGGACATTG 827
Qy 219 eRAsp---TYrProYsg1y 224
Db 828 TCCAGATTACCCAAAGG 847

RESULT 29
AL575307 1102 bp mRNA linear EST 06-APR-2004
LOCUS AL575307 Homo sapiens PLACENTA COR 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0D1061YA20 3-PRIME, mRNA sequence.
ACCESSION AL575307
VERSION AL575307.3 GI:46248266
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 1102)
L1,W.B., Gruber,C., Jessee,J. and Polyes,D.
Full-length cDNA libraries and normalization.
Unpublished (2001)
On Feb 16, 2001 this sequence version replaced gi:31313615.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
into the NotI and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
4941.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?c=CS0D1061B1A10NP1c=4941.f.
FEATURES
source
1..1102
location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
```

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/clone="CS0D1061YA20"
/issue_type="PLACENTA COR 25-NORMALIZED"
/clone_id="Homo sapiens PLACENTA COR 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with NotI and EcoRV and cloned into the NotI and EcoRV
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Alignment Scores:
Pred. No.: 5,55e-95 Length: 1102
Score: 1104.00 Matches: 219
Percent Similarity: 91.67% Conservative: 1
Best Local Similarity: 91.25% Mismatches: 16
Query Match: 84.86% Indels: 6
DB: 1 Gaps: 2

US-10-063-734-122 (1-243) x AL575307 (1-1102)
Qy 4 G1yG1yProAlaA1eSerProG1nAArgLeuAArgG1yLeuLeuLeuLeuLeuG1n 23
Db 1075 CAGGCCCS---CSCCTCCCGACGCGTCCG-----CTCTGCTGTT-CTGYRS 1029
Qy 24 LeuProAlaProSerSerAlaSerG1u1leProYsg1yYsg1yAlaG1nLeuAArg 43
Db 1028 TGCASATGCCCGSCGTCGCGCTTATGATCCCAAGGAAAGCAAAAGCCGACGCTCCGG 969
Qy 44 G1nAArg1yVal1yAAspLeuTYrAenG1yMetCyS1eG1nG1yProAlaG1yValPro 63
Db 968 CAGAGGAGGTGTG-TACCTGTATATGAAATGTCCTTAACAAGGCCACAGCAAGTGCCT 910
Qy 64 G1yAArgApG1ySerProG1yAlaAenVal11leProG1yThProG1y1leProG1yAArg 83
Db 908 GGTCAAGAGCGGAGCCCTGGGSCCAATGSCATTCCGGTACCTCGGATCCCAAGTCCG 850
Qy 84 AAspG1yPheYsg1yG1yUsg1yCysLeuAArgG1yUserPheG1yUgu1ySerTTPThr 103
Db 849 GATGATTCAAAGAGAAAGGAGGAAATGTCGAGGAAAGCTTTGAGAGATCTCGACACA 790
Qy 104 ProAenTYrYsg1yCysSerTTPSerSerLeuAenTYrG1yIleAAspLeuG1yYs1le 123
Db 789 CCCAATCTCAAGACAGTGTTCATGAGATTGATTAATGATGATGATCTTGGGAAATTT 730
Qy 124 AlaG1yCyS1eThPheThYrYMetAArgSerAenSerAlaAenYVal1leuPheSerg1y 143
Db 729 GCGAGGTGACTTTCACAAAGATGCTCAATATAGTCTTAAGATTTTGTCAAGTGC 670
Qy 144 SerLeuAArgLeuYsCyAArgAenAlaCyCySg1yAArgTTPYrPheThrPheAenG1y 163
Db 669 TCACCTTCGCTAAATGACGAATGCAATGCTGTGACGCTGATATTTCACATTCATGGA 610
Qy 164 AlaG1yCySerg1yProLeuPro11eG1yAla1le1leTYrLeuAAspG1nYsg1yPro 183
Db 609 GCTGATGTTTCAGACCTCTCCCATTAAGCTATTAATTTATTTGACCAAGAGGCCCT 550
Qy 184 G1yMeAenSerThYr1leAen11leH1AArgThSerSerValG1yUgu1yCysG1yUgu 203
Db 549 GAAATGAATTCACAAATTAATTAATTCATGCACTTCTCTGAGAGAGACTTGTGAAGGA 490
Qy 204 11eG1yAlaG1yLeuValAAspVala1le1leTTPValG1yThCySerg1yTYrProYs 223
Db 489 ATTTGCTGCGATTTGATGATTTCTATCTGATTTGACATCTTTCATGATTAACCAANA 430
Qy 224 G1yAAspA1eSerThYrTPAenSerValSerAArg1le1le1leG1yUgu1yLeuProYs 243
Db 429 GGAAGATGCTTCACTGATGATGAATTCAGTCTCCATCATTAATTAAGAAAGACTACAAA 370

RESULT 30
AL564395 1064 bp mRNA linear EST 05-APR-2004
LOCUS AL564395 Homo sapiens FETAL LIVER Homo sapiens cDNA clone
DEFINITION CS0D0014YN20 3-PRIME, mRNA sequence.
ACCESSION AL564395
```

VERSION AL564395.3 GI:46231315
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 1064)
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT On Feb 16, 2001 this sequence version replaced gi:31288373.

Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a division of Invitrogen.

This sequence belongs to sequence cluster 4941.f
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?cs=CS0DM014DGI0NP1&c=4941.f.

FEATURES

source

1. 1064
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DM014YN20"
 /issue_type="FETAL LIVER"
 /dev_stage="fetal"
 /clone_lib="Homo sapiens FETAL LIVER"
 /note="Organ: liver; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

ORIGIN

Alignment Scores:

Pred. No.: 5,97e-94 Length: 1064
 Score: 1093.00 Matches: 221
 Percent Similarity: 91.32% Conservative: 0
 Best Local Similarity: 91.32% Mismatches: 17
 Query Match: 84.01% Indels: 8
 DB: 1 Gaps: 2

US-10-063-734-122 (1-243) x AL564395 (1-1064)

QY 3 ProGlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeuLeuLeu 22
 DB 1064 CCCCAGGCCCC---CSCYCCCGCAGGCGCGCC-----CTCTTGTG-CTCTTCTGT 1015
 QY 23 GlnLeuProAlaProSerSerAlaSerGluLeuLeuPolyGlyGlyGlyGlyGly 42
 DB 1014 GCAGCTCCCGCGCGCTGAGCSCTTT-GAGATCCCA-GGGAAGCAAAAGCCAGCTC 957
 QY 43 ArgGlnArgGluValAlaAspLeuTyArgGlyMetCysLeuGlnGlyProAlaGlyVal 62
 DB 956 CGGAGAGGAGGAGT-GTGGACCTGTATATATGATATGCTTAACAAGGCGCAGGAGTG 898
 QY 63 ProGlyArgArgGlySerProGlyAlaAsnValIleProGlyThrProGlyIleProGly 82
 DB 897 CTTGTGTGAAGCGGAGCCCTGGGGCAATGCAATTCGGGTACACTGGGATCCCAAGT 838
 QY 83 ArgAspGlyPheLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 102
 DB 837 CGGGATGATTCAGAGAGAAAGGGGAAATGCTGAGGAGAAAGCTTTGAGAGATCCTGG 778
 QY 103 ThrProAsnTyrlsGlnCysSerTyrSerSerLeuAsnTyrlsGlyIleAspLeuGly 122
 DB 777 ACACCCCACTACAAGCAGTGTTCATGAGTTCATGATATATGCAATGATTCCTTGGGAAA 718

QY 123 IleAlaGluCysThrPheThrIysSerArgSerAsnSerAlaLeuArgValIleuPheSer 142
 DB 717 ATGGGAGTGTACATTTACACATGATGCTTCAATATGCTCTCAAGATTTGTAAAGT 658
 QY 143 GlySerLeuArg-LeuLysCysArgAsnAlaCysCysGlnArgTyrPheThrPheAs 162
 DB 657 GGCTCACTCGCGGCAAAATGCAAAATGCAATGCTGTCAGCGTTGGATTCATCA 598
 QY 162 nGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleTyLeuAspGlnGlySe 182
 DB 597 TGGAGCTGAATCTTACAGACCTCTTCCATGAACTATATATTATTGGACCAAGAG 538
 QY 182 rProGluLeuLeuSerThrIleAsnIleHISArgThrSerSerValGluGlyLeuGly 202
 DB 537 CCTCAAAATGAAATCAACAATTAATTAATTCATCGCACTTCTCTGGAAGCACTTTGTA 478
 QY 202 nGlyIleGlyAlaGlyLeuValAspValAlaIleTyrValGlyThrCysSerAspTyrPr 222
 DB 477 AGGATTTGCTGTGATTAAGATGATGATGCTATCTGGTGGCACTTGTTCAGATTACC 418
 QY 222 OlyGlyAspAlaSerThrGlyTyrAsnSerValSerArgIleIleIleGluGluLeuPr 242
 DB 417 AAAAGAGATGCTCTTCTACTGATGGAATTCAGTCTCTCCATCATTTATTGAAGAACTACC 358
 QY 242 OlyG 243
 DB 357 AAAA 354

RESULT 31

LOCUS

BM915288 1099 bp mRNA linear EST 12-MAR-2002
 AGENCOURT 6702310 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5481457

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE 1 (bases 1 to 1099)
 AUTHORS NIH-MGC http://mgs.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-remail.nih.gov
 Tissue Procurement: DCTD/DTF
 cDNA Library Preparation: Rubin Laboratory
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/BLNM at:
 http://image.jnl.gov

Plate: LLC2005 row: p column: 02
 High quality sequence start: 26
 High quality sequence stop: 565.
 Location/Qualifiers
 1. 1099

FEATURES

source

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5481457"
 /tissue_type="amelanotic melanoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 41"
 /note="Organ: skin; Vector: pOT87; Site 1: XhoI, Site 2: EcoRI, cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCGAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC library."

ORIGIN

Alignment Scores:

Pred. No.:	1.55e-90	Length:	1099.
Score:	1057.50	Matches:	212
Percent Similarity:	92.80%	Conservative:	7
Best Local Similarity:	89.83%	Mismatches:	8
Query Match:	81.28%	Indels:	9
DB:	4	Gaps:	2

US-10-063-734-122 (1-243) x BM915288 (1-1099)

```

QY 1 MetArgProGlnGlyProAlaAspSerProGlnArgGlyLeuLeuLeuLeu 20
DB 99 ATGCCAGCCCGAGGGCCCGCCCTCCCGCAGCGGCTCCGGGCTCTGCTGCTCCG 158
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluLeuProGlyGlyVala 40
DB 159 CTGCTGCAAGCTCCCGCCGCTCGAGCCGCTCTGAGATCCCAAGGGAGCAAGGCG 218
QY 41 GlnLeuArgGlnArgGluValValAspLeuTyrAspGlyMetCysLeuGlnGlyProAla 60
DB 219 CAGCTCCGCGCAGAGGAGGTGGTGAAGCTGTATTAATGATGTCTTACAGGGCCAGCA 278
QY 61 GlyValProGlyArgAspGlySerProGlyValaAsnValIleProGlyThrProGlyIle 80
DB 279 GGAAGTCCCTGCTCGAGACCGGACCCCTGGGGCCATGGCATTCGGGTCACCTGGGATC 338
QY 81 ProGlyArgAspGlyPheLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100
DB 339 CCAGTCCGCGAGTGAATTCAAGAGAAAGGGGGAATGCTGAGGGAAAGCTTTGAGAG 398
QY 101 SerTPThrProAsnTyrIleGlnCysSerTyrSerSerLeuAsnTyrIleLeuLeu 120
DB 399 TCTTGACACCCCACTACCAAGAGAGTGTATGATGATGATGATGATGATGATGATGAT 458
QY 121 GlyValIleAlaGluCysThrPheThrIleMetArgSerAsnSerAlaLeuArgValLeu 140
DB 459 GGGAAATGTCGAGAGTGCATTTTACAAAGATGCTTCAAAATGATGCTTCAAGAGTTTG 518
QY 141 PheSerGlySerLeuArgLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 160
DB 519 TTCAGTGCTCACTTCGCTCAAAATGCAAAATGCAATGCAATGCAATGCAATGCAAT 578
QY 161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGluValIleIleLeuLeuAspGln 180
DB 579 TTCATGAGCTGAATGTTCAAGACCTCTCCCTTGAAGCTATATATTATTTGACCAT 638
QY 181 -GlySerProGlnMetAsnSerThrIleAsnIleHisArg-ThrSerSerValGluGly 200
DB 639 AGAAACCCCTGAAATGGATTTCCAACTTAAATTTCTCCCAACTTCTTCTGGGGAGAGC 698
QY 200 euCyGluGluGlyIleGlyAlaGlyLeuVal-AspValAlaIleLeu-----ValGly 216
DB 699 TTTGTGAAGAATTTGGCGCTGATTATATGAGATGTTGCTATCTGGGGTTGGCAACTGGT 758
QY 217 ThrCysSerAspTyrProGlyGlyAsp-AlaSerThrGly 229
DB 759 -----TCAATTAACCAAAAGGGAGATCTTCCACAGCGG 792

```

RESULT 32
 LOCUS B0574527/c 617 bp mRNA linear EST 19-JUN-2002
 DEFINITION UI-H-E21-dba-e-10-0-UI.s1 NCI CGAP Ch2 Homo sapiens cDNA clone
 UI-H-E21-dba-e-10-0-UI 3', mRNA sequence.
 ACCESSION B0574527
 VERSION B0574527.1 GI:21477837
 KEYWORDS EST.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 617)

AUTHORS

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

JOURNAL

Unpublished (1997)

COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. Steven Gilelis/ Rush Presbyterian, Dept. of
 Orthopaedics
 cDNA library preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be obtained
 from Dr. M. Bento Soares, bento-soares@iowa.edu
 The following repetitive elements were found in this cDNA
 sequence: 1-28, >AT rich#low_complexity
 Seq primer: M13 FORWARD
 POLYA=yes.

FEATURES

source

Location/Qualifiers
 1..617
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-H-E21-dba-e-10-0-UI"
 /tissue_type="Chondrosarcoma Grade II"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /clone_id="NCI CGAP Ch2"
 /note="Organ: Left Pelvis; Vector: pRTT3-Pac (Pharmacia)
 with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
 NCI CGAP Ch2 is a normalized cDNA library containing the
 following tissue(s): Chondrosarcoma Grade II. The library
 was constructed according to Bonaldo, Lennon and Soares,
 Genome Research, 6:791-806, 1996. First strand cDNA
 synthesis was primed with an oligo-dT primer containing a
 Not I site. Double stranded cDNA was ligated to an EcoR I
 adaptor, digested with Not I, and cloned directionally
 into pRTT3-Pac vector. The oligonucleotide used to prime
 the synthesis of first-strand cDNA contains a library tag
 sequence that is located between the Not I site and the
 (dT)18 tail. The sequence tag for this library is
 TGAATCAGCT.
 TAG TISSUE=grade-2-chondrosarcoma
 TAG LIB=UI-H-E21
 TAG_SEQ=ATCTAATATG"

ORIGIN

Alignment Scores:

Pred. No.:	1.57e-88	Length:	617
Score:	1033.00	Matches:	191
Percent Similarity:	98.45%	Conservative:	0
Best Local Similarity:	98.45%	Mismatches:	2
Query Match:	79.40%	Indels:	1
DB:	5	Gaps:	0

US-10-063-734-122 (1-243) x B0574527 (1-617)

```

QY 51 TYRAsnGlyMetCysLeuGlnGlyProAlaGlyValProGlyArgAspGlySerProGly 70
DB 616 TATTAATGGAATGTCTTACCAAGGGCCAGAGAGTGGCTGTGCGAGACGGAGCCCTGGG 557
QY 71 AlaAsnValIleProGlyThrProGlyIleProGlyArgAspGlyPheLeuGlyGlyLeu 90
DB 556 GCCAATGGCATTCGCGGTCACCTGGATCCAGATCGGATGATTTCAAGAGAGAAAG 497
QY 91 GlyGluCysLeuArgGlySerPheGluGlySerTyrThrProAsnTyrIleGlnCysSer 110
DB 496 GGGGAATGTCTGAGGAAAGCTTTGAGGAGCTCTGAGACCCCACTACAGACAGCTTCA 437
QY 111 TTPSerSerLeuAsnTyrGlyIleAspLeuGlyValIleAlaGluCysThrPheThrIle 130
DB 436 TGGAGTTTATGAATTAATGAGCATATGCTTGGGAAATTCGCGAGTGTACATTTCAAG 377
QY 131 MetArgSerAsnSerAlaLeuArgValLeuPheSerGlySerLeuArgLeuLeuLeu 150

```

Db 376 ATGGCTCAATATAGCTCTAAGAGTTTGTTCAGTGGCTACTTCGGCTAAATGAGA 317
 Qy 151 AAmLaAcyScySgLnAgtTPTyPheThrpheanSgLnAglAcySserGlyProLeu 170
 Db 316 AATGCAATGCTGCGCTGTGTATTCATTCATGAGTGAATGTTGAGAGCTCTT 257
 Qy 171 ProilegLuAAlaileTyLeuAAspGlnGlySerProGluMetAAsnSerThrIleAsn 190
 Db 256 CCATTAGAGCTATATTTATTTGACCAAGAAAGCCCTGAAATTCACACATTAAT 197
 Qy 191 ILeHsArGThrSerSerValGluGlyLeuCySgLnGlyIleGlyAlaGlyLeuValAsp 210
 Db 196 ATTCATCGCACTTCTCTGTGAAGAGACTTGTGAAGAAATGGCTGCTGATTTAGTCAT 137
 Qy 211 ValAlaIleTrpValGlyThrCySerSerAspTyPro-LysGlyAAspAlaSerThrGlyTr 230
 Db 136 GTTGCCTATCGGGTGGACCTGTTCAGATTACCCAAAAGAGATGCTTCTACTGGATG 77
 Qy 230 PaenSerValSerArgIleIleIleGluGluLeuProLys 243
 Db 76 GAATTCAGTTTCTCGCATCATTTATTAAGAACTAACCCAA 37

RESULT 33
 B0648112 986 bp mRNA linear EST 15-JUL-2002
 LOCUS AGENCOURT_8507019 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:6297812
 DEFINITION 5', mRNA sequence.
 ACCESSION B0648112
 VERSION B0648112.1 GI:21772284
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 986)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: CGAP (Stanford)
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLN at:
 http://image.llnl.gov
 Plate: L1CM2507 row: n column: 21
 High quality sequence stop: 520.
 Location/Qualifiers
 1..986
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6297812"
 /issue_type="hepatocellular carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NTH MGC_100"
 /note="Organ: liver; Vector: pOT87; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGACGAG(G). Size-selected >500bp for average insert size
 1.8kb. Library constructed by Ling Hong in the laboratory
 of Gerald M. Rubin (University of California, Berkeley)
 using ZAP-cDNA Synthesis Kit (Stratagene) and Superscript
 II RT (Life Technologies). Note: this is a NIH_MGC
 Library."

ORIGIN
 Alignment Scores:
 Pred. No.:
 Score:

5,79e-87 Length: 986
 1019.50 Matches: 208

Percent Similarity: 88.33%
 Best Local Similarity: 86.67%
 Query Match: 78.35%
 DB: 5
 Gaps: 3

US-10-063-734-122 (1-243) x B0648112 (1-986)

Qy 1 MetArProGlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeuLeu 20
 Db 102 ATGCACCCCAAGGCGCCCGCTCCCGAGGCGCTCCGCGCTCTGCTGCTCTG 161
 Qy 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluIleProLysGlyLeuValAsp 40
 Db 162 CTGCTGAGCTGCCCGCCGCTCGAGCGCTCTGAGATCCCAAGGGAAGCAAGGCG 221
 Qy 41 GlnLeuArgGlnArgGlnValAlaAspLeuTyTrpAsnGlyMetCySgLnGlyProAla 60
 Db 222 CAGCTCCGCGAAGAGAGGTGTGACCTGTATTAAGAAATGCTTACAGGCGCAGCA 281
 Qy 61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
 Db 282 GAGTGCCTGTGAGAGCGGAGCCCTGGGCGCAATCGCATTCGGGTACCTGGAGAT 341
 Qy 81 ProGlyArgAspGlyPheLysGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100
 Db 342 CCAAGTCGGAGTGTATTCAAAGAGAAAGGGGGAATGCTGAGGGAAGCTTTGAGGAG 401
 Qy 101 SerTrpThrProAsnTyTrpLysGlnCySerTrpSerSerLeuAsnTyGlyIleAspLeu 120
 Db 402 TCTTGACACCAACCACTCAAGAGCTGTATGAGTTCTTAATTAATGCAATGATCTT 461
 Qy 121 GlyValIleAlaGluCyThrPheThrLysMetArgSerAsnSerAlaLeuArgValLeu 140
 Db 462 GGGAAATTCGAGAGGTATCAATTAACAAGAGCGCTTCAATATGCTTAAGAGTTTG 521
 Qy 141 PheSerGlySerLeuArgLeuLysCySgLnAlaCySgLnArgTrpTyPheThr 160
 Db 522 TTCAAGTGCCTCACTTGGCTTAATCAAAATGCAATGCTGACAGCTGTGATTTGACA 581
 Qy 161 PheAsnGlyAlaGluCySerGlyProLeuProIleGluAlaIleIleTyLeuAspGln 180
 Db 582 TTCAATGAGCTGAATGTTACAGACCTCTCCCATTTGAAGCTAATATTATTGGACCA 641
 Qy 181 GlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerVal---GluGly 199
 Db 642 CGAAGCCTGGAATGATTCACCAATATATTTCTCGCACTTCTGTGGGAAGA 701
 Qy 199 yLeuCySgLnGlyIle-GlyAlaGlyLeu-ValAspValAlaIle---TrpValGly--- 216
 Db 702 CTTTGTGAAGAAATGGGGCTGGAATTAAGTGAATGTGCTATTCCTGGGGTTGGGCAC 761
 Qy 217 ThrCySerSerAspTyProLysGlyAlaSerThrGlyTrpPaenSerValSer 234
 Db 762 TTGCTTCAGAAATTAACCCAAAAGAAAGATGCTTCTACTGAGATGAAATTC 815

RESULT 34
 AL585129 890 bp mRNA linear EST 28-FEB-2001
 LOCUS ROS019808, mRNA sequence.
 DEFINITION ROS019808, mRNA sequence.
 ACCESSION AL585129 GI:1163862
 VERSION AL585129.1 GI:1163862
 KEYWORDS EST.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 REFERENCE 1 (bases 1 to 890)
 AUTHORS Murray, F.
 TITLE BP Chicken Embryo Library
 JOURNAL Unpublished (2001)
 COMMENT Contact: Frazer Murray


```

Db      118  CCCAGCGCGCTCCCGGAGCGGAGACCTCGAACCACGCGGATCCCGGAGACCG
Qy      79  G1Y1LePProG1YArGAspG1YPhelYsg1Yg1uYsg1Yg1uYsleuAArg1uSerPhe
Db      178  GGGATCCCGGGCGCGGAGCGGCGCCAAAGGAGAAAGGCGAGTCTTGGCGGAGACAT
Qy      99  G1UG1uSerTrpThrProAsnTrpLysGlnCysSerTrpSerSerLeuAsnTrpY11e
Db      238  GAGAGAGTCTCGAGCGCCCACTTCACAGACAGTGTGCGAGCGCAGCTACGCGGATA
Qy      119  AsPleuG1YpYs11e1aG1uYsTrpPheThrLysMetLysSerAsnSerAlaLeuArg
Db      298  GACCTGGGAGAAATAGCGGAGATGACCTTCACAAAGATGGCTCCACACAGTGTCTCAGA
Qy      139  Val1euPheSerSerg1YsleuAArgLeuLysCysArgAsnAlaCysCysGlnAArgTrpY1
Db      358  GTCCTTTTCAGTGGATCGCTCCGCGTGAAGTCGCGAAGCCCTGTCTCAGCCCTGGTAC
Qy      159  PheThrPheAsnG1YAlaG1uYsSerG1YProLeuPro11eG1uA11e11eY11eY11e
Db      418  TTCACCTTCATGATGAGAGATGCGCGGCGCACCTTCCATCGAAGCCATATATATTTA
Qy      179  AsP1uG1YsErProG1uMetAsnSerThrL1eAsn11eH1sArgThrSerSerValG1u
Db      478  GATCAAGGACGATCGGAGACTGACATCTATCATCAACATACCGAAGCTCTCAGTGAA
Qy      199  G1YLeuCYeG1uG1Y11eG1YAlaG1YLeuValAspValA11e11eTrp-ValG1YThrCY
Db      538  GGTCTGGTGAAGGAGATCAACGCTGTGTGATCATCGCATCTGAGATCGGAGCTTG
Qy      218  sSerAsP1YrProLysG1YAspAlaSerThrG1YTPAsnSerValSerArg11e11e
Db      598  CTCTGACTCTCCCGAGGAGATGCTTCTACTGATGAGATTCAGTCTCCGATCATCAT
Qy      238  eG1uG1uLeu 241
Db      658  TGAAGAACTA 667

```

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RESULT 36  CN394776 700 bp mRNA linear EST 16-MAY-2004
LOCUS      CN394776
DEFINITION 1700042453311 GRN_EB Homo sapiens cDNA 5', mRNA sequence.
ACCESSION  CN394776
VERSION     CN394776.1 GI:47382371
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   1  Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
AUTHORS     Li, Y., Xu, C., Fang, R., Guebler, K., Rao, M.S., Mandeljam, R.,
            Lebkowski, J. and Stanton, L.W.
            Transcriptome characterization elucidates signaling networks that
            control human ES cell growth and differentiation
            Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT     Contact: Brandenberger R
            Regenerative Medicine
            Genon Corporation
            230 Constitution Drive, Menlo Park, CA 94025, USA
            Tel: 650 473 8658
            Fax: 650 473 7760
            Email: rbrandenberger@genon.com
            Insert Length: 700 Std Error: 0.00.
            Location/Qualifiers
            1. 700
FEATURES
    source
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /tissue_type="embryonic stem cells, embryoid bodies
        derived from H1, H7 and H9 cells"
        /clone_1b="GRN_EB"

```

ORIGIN

Alignment Scores:

```

Pred. No.: 1.25e-84
Score: 993.00
Percent Similarity: 99.46%
Best Local Similarity: 99.46%
Query Match: 76.33%
DB: 7

```

/note="oligo dT primed, full-length enriched cDNA library from embryoid body outgrowths derived from hES cell lines H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free conditions."

US-10-063-734-122 (1-243) x CN394776 (1-700)

```

Qy      1  MetArgProG1uG1YProAla1a1aSerProG1uArgLeuArgG1YLeuLeuLeuLeu 20
Db      142  ATGGAGCCCGAGGCGCGCGCGCTCCCGCAGCGGCTCCGCGGCTCTGCTGCTCTG 201
Qy      21  LeuLeuG1uLeuProAlaProSerSerAlaSerG1u11eProLysG1YysG1uYsAla 40
Db      202  CTGCTGAGCTGCCCGCGCGCGCTGAGCGCTCTGAGATCCCGAAGGAGAAAGAGGG 261
Qy      41  G1uLeuArgG1uArgG1uVala1a1aSerLeuY11eArgG1YMetCysLeuG1uG1YProAla 60
Db      262  CAGCTCCGCGAGAGGAGGAGTGTGAGCTGTATATATGATGTGCTTACAGGGCGACCA 321
Qy      61  G1YAlaProG1YArgAspG1YsErProG1YAlaAsnVal11eProG1YThrProG1Y11e 80
Db      322  GGAATGCTGTGTGAGAGCGGAGCCCTGGGGCCAAATGAGCATTCGGGTACCTGGATC 381
Qy      81  ProG1YArgAspG1YpYsG1Yg1Yg1Yg1Yg1Yg1Yg1Yg1Yg1Yg1Yg1Yg1Yg1Y 100
Db      382  CCAAGTGGAGATGATTCAAAGGAGAAAGGGGAGATGTCTAGGAGAAAGCTTGAAGAG 441
Qy      101  SerTrpThrProAsnTrpLysGlnCysSerTrpSerSerLeuAsnTrpG1Y11eAspLeu 120
Db      442  TCTGAGACCCCAACTACAAAGAGAGTTCATGAGATTCATTAATTAATGCAATGATCTT 501
Qy      121  G1Y1Y11e1a1aG1uYsThrPheThrLysMetArgSerAsnSerAlaLeuArgVal11e 140
Db      502  GGGAAATATCGGAGAGTCAATTCATTAAGAGCCCTCAATATAGCTCTAAGAGTTTG 561
Qy      141  PheSerG1YsErLeuArgLeuLysCysArgAsnAlaCysCysGlnAArgTrpTrpPheThr 160
Db      562  TTCAGTGGCTCACTTGTGCTTAATGCAAGATGATCTGTGAGTGTGATTTTCA 621
Qy      161  PheAsnG1YAlaG1uYsSerG1YProLeuPro11eG1uA11e11eY11eY11eY11eY11e 180
Db      622  TTCAAATGAGCTGATGTTCAAGACCTCTCCCATTAAGCTATTAATTTTGGACCA 681
Qy      181  G1YsErProG1uMetAsn 186
Db      682  GGAAGCCCTGAATATGAT 699

```

```

RESULT 37  BU408973 765 bp mRNA linear EST 29-NOV-2002
LOCUS      BU408973
DEFINITION 603159022F1 CSEORBL03 Gallus gallus cDNA clone CHEST17715 5', mRNA
ACCESSION  BU408973
VERSION     BU408973.1 GI:25901644
KEYWORDS    EST.
SOURCE      Gallus gallus (chicken)
ORGANISM    Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
            1 (bases 1 to 765)
REFERENCE   1  Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
AUTHORS     Ford, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
            A Comprehensive Collection of Chicken cDNAs
TITLE

```


compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., EMAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

ORIGIN

Alignment Scores:

Pred. No.:	1-71e-82	Length:	681
Score:	970.50	Matches:	183
Percent Similarity:	88.55%	Conservative:	18
Best Local Similarity:	80.62%	Mismatches:	22
Query Match:	74.60%	Indels:	4
DB:	5	Gaps:	2

US-10-063-734-122 (1-243) x BU278868 (1-681)

```

QY 4 GlnGlyProAlaIaIaSerProGlnArgLeuArgGlyLeuLeuLeuLeuLeuGln 23
DB 7 CGAGAGAGGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 66
QY 24 LeuProAlaIaIaProSerSerAlaSerGlnIleProGlyGlyGlyGlyGlyGly 43
DB 67 CTG-----GGCTCGGGGCTCGCGGACAGCCCGCGGACAAAGAGG---GGCGG 117
QY 44 GlnArgGlnValValAspLeuIleYranGlyMetCysLeuGlnGlyProAlaGlyValPro 63
DB 118 CGCGGAGAGGTGCTGTCGACGAGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 177
QY 64 GlyArgAspGlySerProGlnAlaAsnValIleProGlyThrProGlyIleProGlyArg 83
DB 178 GAGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 237
QY 84 AspGlyPheGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 103
DB 238 GACGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 297
QY 104 ProAsnIleYranGlySerSerProGlnAlaIleIleYranGlyGlyGlyGlyGly 123
DB 298 CCCAATTCAACAGTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 357
QY 124 AlaGlnCysThrPheThrIleMetArgSerSerSerSerSerSerSerSerSerSer 143
DB 358 GCGGATATGATCTTCAAAAGATGCGCTCAACAGTCTTCAAGTCTTCAAGTCTT 417
QY 144 SerLeuArgLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 163
DB 418 TCGCTCGGCTGAAAGTCCGGAAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 477
QY 164 AlaGlnCysSerGlyProLeuProIleGlnAlaIleIleYranGlyGlyGlyGly 183
DB 478 GCAAGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 537
QY 184 GlnMetLeuSerThrIleAsnIleIleIleIleIleIleIleIleIleIleIleIle 203
DB 538 GAACTGAACCTTACTATCAACATACCGAAGTCTTCAAGTCTTCAAGTCTTCAAG 597
QY 204 IleGlyIaGlyLeuValAspValAlaIleThrValGlyThrCysSerAspIlePro 223
DB 598 ATCAACCGTGGCTTGGTGACATCGCCATCTGGAGCTGCTGCTGCTGCTGCTGCT 657
QY 223 GgIAspAlaIaSerThrGly 229
DB 658 GGGCGATGCTTCTACTGG 676

```

RESULT 39
LOCUS CB959810
DEFINITION CB959810 798 bp mRNA linear EST 29-Apr-2003
ACCESSION CB959810
VERSION CB959810.1 GI:30215926

KEYWORDS

EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 798)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM384 row: h column: 13
High quality sequence stop: 496.
Location/Qualifiers

COMMENT

FEATURES

source

```

1..798
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30345876"
/class_type="Human Placenta"
/lab_host="DH10B TONa"
/clone_id="NIH MGC 147"
/note="Organ: Placenta; Vector: pBluescriptR, Site 1:
all-XhoI, Site 2: BamH; Oligo-dT primed using primer
insert size 2.3 kb and normalized to R0T 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
NIMH/NHGRI, National Institutes of Health). Note: This is
a NIH-MGC library."

```

ORIGIN

Alignment Scores:

Pred. No.:	2.12e-82	Length:	798
Score:	970.50 <td>Matches:</td> <td>196</td>	Matches:	196
Percent Similarity:	83.97%	Conservative:	3
Best Local Similarity:	82.70%	Mismatches:	13
Query Match:	74.60%	Indels:	25
DB:	6	Gaps:	3

US-10-063-734-122 (1-243) x CB959810 (1-798)

```

QY 1 MetArgProGlnGlyProAlaIaIaSerProGlnArgLeuArgGlyLeuLeuLeu 20
DB 98 ATCGAGACCCGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 157
QY 21 LeuLeuGlnLeuProAlaIaIaProSerSerAlaSerGlnIleProGlyGlyGly 40
DB 158 CTGCTGCGAGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 217
QY 41 GlnLeuArgGlnArgGlnValValAspLeuIleYranGlyMetCysLeuGlnGly 60
DB 218 CAGCTCCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 277
QY 61 GlyValProGlyArgAspGlySerProGlyValAlaAsnValIleProGlyThrPro 80
DB 278 GGAATGCTGCTGTCGAGACGGAAGCTCGGGCCAAATGCAATTCGGGTCACCTG 337
QY 81 ProGlyArgAspGlyPheGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100
DB 338 CCAAGTCCGAGTGAATTCAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 397
QY 101 SerThrProAsnIleYranGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 120

```


[illegible]

```

FEATURES
SOURCE

location/Qualifiers
1. 570
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="gcal0015c.e.21"
/tissue_type="multi-tissues"
/dev_stage="from embryos to adults"
/lab_host="DH108"
/clone_lib="AGENAS Gallus gallus multi-tissues normalized
and once-subtracted cDNA library (gcal)"
/notes="Vector: pRTT3D-pac; tissues: adipose tissue, brain,
kidney, liver, multi-tissues, muscle, ovary, testis, bone
marrow, caecum, duodenum, embryos, fabricius gland,
granulosa, hypochlamys, ileon, jejunum, oviduct,

```

pancreas, skin, spleen, thymus, utero-vaginal gland, pituitary gland, hematopoietic progenitor cells, small follicle. Clonal distribution: AGENAS, Resource Centre, Follicle PIUMI, Francis Piumi, INRA, CEA Radiobiologie et Etude du genome (URB5), Domaine de Valvert, 78352, Jouy-en-Josas cedex, FRANCE"

Alignment Scores:

Pred. No.:	7,92e-81	Length:	578
Score:	952.00	Matches:	176
Percent Similarity:	96.26%	Conservative:	10
Best Local Similarity:	90.91%	Mismatches:	7
Query Match:	73.17%	Indels:	0
DB:	5	Gaps:	0

US-10-063-734-122 (1-243) x BX265931 (1-570)

[illegible]

Pred. No.: 1.88e-80 Length: 995
 Score: 951.50 Matches: 192
 Percent Similarity: 80.23% Conservative: 15
 Best Local Similarity: 74.42% Mismatches: 17
 Query Match: 73.14% Indels: 37
 DB: 5 Gaps: 2

US-10-063-734-122 (1-243) x BUI141753 (1-995)

QY 19 LeuLeuLeuLeuLeuLeuProAlaProSerSerAlaSerGluIleProlyGlyLysGln 38
 DB 14 CTGCTGCTCTGCGCCCTGCTGCTGCGGCGCTCGCCGACGCGCCGACGCGCGGCGGCAAAACAG 73
 QY 39 LysAlaGlnLeuArgGlnArgGlnValValAspLeu----- 50
 DB 74 CGAGCG---CGCGGCGCGGAGGCTGAGAGC-GGTCTGTTCTCTGCTGGAACA 129
 QY 50 ----- 50
 DB 130 TTTTCTCACTCATCTGGAAGCATTAGCTTTCCACTGCTCTGCGGCTTCACTT 189
 QY 51 -----TyrAsnGlyMetCysLeuGlnGlyProAlaGlyValProGlyArg 65
 DB 130 GAGCACTGCTGCTGAGTACAAAGCGCGCTGCTGCAAGGCGCCGACGCGCTCCCGGAGCG 249
 QY 66 AspGlySerProGlyValAsnValIleProGlyTyrProGlyTyrLeuProGlyArg 85
 DB 250 GAGCGGAACCTGGAACCAACGCG-GATCCCGGAGACCGCGGAGTCCCGGCGGAGCGG 308
 QY 86 PheLysGlyGlnLysGlyLysGlyCysLeuArgGlySerPheGlyGlySerTyrPro 105
 DB 309 CCCAAAGGGGAAAGGCGCAGTCTTGGCGGAGAGCATTAGAGAGCTCTGAGACGCCAAC 368
 QY 106 TyrLysGlnCysSerTyrSerSerLeuAsnTyrGlyIleAspLeuGlyLysIleAlaGln 125
 DB 369 TTCAAGCAGTGTCTCGGAGAGCGACTGAGACTAGCGGATAGACTGGGAAATAGCGGAA 428
 QY 126 CysThrPheThrLysMetLysSerAsnSerAlaLeuArgValLeuPheSerGlySerLeu 145
 DB 429 TGTAGCTTCAAAAGATGGCTCTCCAAAGTCTCTCAAGTCTCTTTCAGTGTGATGCTC 488
 QY 146 ArgLeuLysCysArgAsnAlaCysCysGlnArgTyrPheThrPheAsnGlyAlaGln 165
 DB 489 CGGCTGAAAGTCCGAAAGCCCTCTCTCAAGCGCTGACTTCACTTCAATGAGAGAA 548
 QY 166 CysSerGlyProLeuProIleGluAlaIleIleTyrLeuAspGlnGlySerProIleMet 185
 DB 549 TCGCGCGGCGCACTTCCATCGAAGCCATATATATTAGATCAAGGAGTCCGGAAC 608
 QY 186 AsnSerThrIleAsnIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 205
 DB 609 AACTCTACTATCAAACTACCAAGCCTCTCAAGTGAAGTCTGTGTAAGGAGCAAC 668
 QY 206 AlaGlyLeuValAspValAlaIleTyrValGlyTyrCysSerAspTyrProlyGlyAsp 225
 DB 669 GCTGGCTGTGAGACATCCCATCTGGGTGCGGACTTGGCTGACTACCAACCG-AGAGAT 727
 QY 226 AlaSerThrGlyTyrAsnSerValSerArgIleIleIleGlnGluLeuProIle 243
 DB 728 GCTTCTACTAGATGAAATCAGTCTCCCGATCATCATGAAAGAACTGCCAAA 781
 RESULT 43
 BE896915 688 bp mRNA linear EST 20-OCT-2000
 LOCUS 60139437F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924560 5',
 DEFINITION mRNA sequence.
 ACCESSION BE896915
 VERSION BE896915.1 GI:10361827
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 688)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: ATCC/DCRP
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: LLM9762 row: 1 column: 09
 High quality sequence stop: 685.
 Location/Qualifiers

FEATURES

source

1. 688
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3924560"
 /issue_type="melanotic melanoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 72"
 /note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 2 kb. Library constructed by Life
 Technologies."

ORIGIN

Alignment Scores:

Pred. No.: 5.39e-79 Length: 688
 Score: 934.00 Matches: 185
 Percent Similarity: 97.88% Conservative: 0
 Best Local Similarity: 97.88% Mismatches: 3
 Query Match: 71.79% Indels: 3
 DB: 2 Gaps: 0

US-10-063-734-122 (1-243) x BE896915 (1-688)

QY 1 MetArgProGlnGlyProAlaAlaSerProGlnArgLysGlyLeuLeuLeuLeu 20
 DB 117 ATGGACCCCAAGAGGCGCGCGCTCCCGGAGCGGCTCCGCGCTCTGCTGCTCG 176
 QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluIleProlyGlyLysGlnLysAla 40
 DB 177 CTGCTGAGCTGCGCGCGCGCTGAGCGCTCTGAGATCCCAAGGGAAGCAAGCGG 236
 QY 41 GlnLeuArgGlnArgGlnValValAspLeuTyrAsnGlyMetCysLeuGlnGlyProAla 60
 DB 237 CAGCTCCGCAAGGAGGAGGTGAGCTGTATATGGAATGCTTACAGGCGCAGCA 296
 QY 61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
 DB 297 GGAAGTCCGTGTCGAGAGCGAGCCCTGGGCAATGGAATCCGGGTACACTGGAGATC 356
 QY 81 ProGlyArgAspGlyPheLysGlyGlyLysGlyCysLeuArgLysPheGlnGlu 100
 DB 357 CCAGGTCCGAGATGATTCAAAGAGAAAAGGGGGAATGCTAGAGGAAGCTTTGAGGAG 416
 QY 101 SerTPMPProAsnTyrLysGlnCysSerTyrSerSerLeuAsnTyrGlyIleAspLeu 120
 DB 417 TCTTGACACCCCACTACAGAGAGTTCATGAGTTCACTTAATTAATGCAATGATCTT 476
 QY 121 GlyLysIleAlaGlnCysThrPheThrLysMetArgSerAsnSerAlaLeuArgValLeu 140
 DB 477 GGAATAATGGGAGGTATCATTTCAAAAGAGCGCTTCAATATGCTCTAAGAGT-TTG 535
 QY 141 PheSerGlySerLeuArgLeuLysCysArgAsnAlaCysCysGlnArgTyrPheThr 160
 DB 536 TTCAGTGGCTCACTTCGCTAAATGCAAGAAATGATGCTGCAAGC-TGGTATTTTCA 594
 QY 161 PheAsnGlyAlaGlnCysSerGlyProLeuProIleGluAlaIleIleTyrLeuAspGln 180

sequence.
Plate: 0050 row: h column: 6
Seq primer: M13R.

FEATURES
source
Location/Qualifiers

1..790
/organism="Onchocerca mykiss"
/mol_type="mRNA"
/db_xref="taxon:8022"
/clone="tcdbk0050c.h.06"
/issue_type="multi-issues"
/dev_stage="from embryos to adults"
/lab_host="DH10B"
/clone_1ib="tcdbk"
/note="Vector: pT73D-pac; AGENAE Rainbow trout
multi-issues - normalized + 2 subtractions; Clone
distribution : AGENAE Resource centre, Francois PIUMI,
Francois Plumiojouy.lnra.fr, INRA, CEA Radiobiologie et
Etude du genome (URBG), Domaine de Vilvert, 78352,
Jouy-en-Josas cedex, FRANCE, +33 (0) 1.34.65.28.02, +33
(0) 1.34.65.22.73"

ORIGIN

Alignment Scores:
Pred. No.: 2,466-77 Length: 720
Score: 917.50 Matches: 166
Percent Similarity: 89.32% Conservative: 18
Best Local Similarity: 80.58% Mismatches: 21
Query Match: 70.52% Indels: 1
DB: 5 Gaps: 1
US-10-063-734-122 (1-243) x BX84616 (1-790)

OY 38 GlnlyAAGlnleuAArglnAArglnAValAAspLeuTyrAAsnGlyMetCysLeuGln 57
Db 1 AGAAAGGCACTTGACAGAGAGATGTTGAATACGAAAGTACACAGC---TGCCCCCG 57
OY 58 GlyProAlaGlyValProGlyAArgAAspGlySerProGlyAlaAsnValIleProGlyThr 77
Db 58 GGTCCGGCTGCAACCCCTGGAAGAGGTAACCTCGACCAATGGCTCCCTGGACT 117
OY 78 ProGlyIleProGlyAArgAAspGlyPheGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 97
Db 118 CCGGCGATCCCGGGGCGATGATGATCAAGGGGAGAAAGAGAGTGTGATGATGATG 177
OY 98 PheGlnGlnSerTyrThrProAAsnTyrGlnCysSerTyrSerSerIleuAAsnTyrGly 117
Db 178 TTGAGAGACCATGAAACCACTACAGAGTGTGATGATGATGATGATGATGATGATG 237
OY 118 IleAAspLeuGlyIleAAspLeuGlyIleAAspLeuGlyIleAAspLeuGlyIleAAsp 137
Db 238 ATGACCTGGGCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 297
OY 138 ArgValIleuPheSerGlySerLeuAArgLeuGlyCysAArgAAsnAlaCysCysGlnAArg 157
Db 298 CGTGTGCTCTTCAGAGGCTCCCTGAGGCTGAAGTGAAGACAGCCTGCTGCTGCTGCTG 357
OY 158 TyrPheThrPheAAsnGlyAAsnGlyCysSerGlyProLeuProIleGlnAlaIleIleTyr 177
Db 358 TACTTCACTTCACAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 417
OY 178 LeuAAspGlnGlySerProGlyIleuAAspLeuGlyIleAAsnIleAAsnIleAAsnIle 197
Db 418 CTCGACCAAGGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 477
OY 198 GlnGlyLeuGlyGlnGlyIleGlyAAsnGlyLeuValAAspValAlaIleTyrValGlyThr 217
Db 478 GAAGGCTGTGTGAGGAGATCCGGGAGGCTGCTGATGATGATGATGATGATGATGATGATG 537
OY 218 CysSerAAspTyrProGlyAAspAAsnTyrGlyTyrAAsnSerValSerAArgIleIle 237
Db 538 TGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 597
OY 238 IleGlnGlnLeuProlys 243

Db 598 ATAGAGAGCTGCCAAA 615

FEATURES

RESULT 46
CN394775 571 bp mRNA linear EST 16-MAY-2004
LOCUS 1700532586464 GRN_EB Homo sapiens cDNA 5', mRNA sequence.
DEFINITION CN394775
ACCESSION CN394775
VERSION CN394775.1 GI:47382370
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 571)
Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Pisk, G.J.,
Li, Y., Xu, C., Pang, R., Guegler, K., Rao, M.S., Mandalam, R.,
Lebkowski, J. and Stanton, L.W.
Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 571 Std Error: 0.00.
Location/Qualifiers

ORIGIN

1..571
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, embryoid bodies
derived from H1, H7 and H9 cells"
/clone_1ib="GRN_EB"
/note="Toligo dT primed, full-length enriched cDNA library
from embryoid body outgrowths derived from hES cell lines
H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
conditions."

FEATURES

Alignment Scores:
Pred. No.: 1,776-77 Length: 571
Score: 917.00 Matches: 170
Percent Similarity: 99.42% Conservative: 0
Best Local Similarity: 99.42% Mismatches: 1
Query Match: 70.48% Indels: 0
DB: 7 Gaps: 0
US-10-063-734-122 (1-243) x CN394775 (1-571)

OY 1 MetAAspProGlnGlyProAlaAAspProGlnAArgLeuAArgGlyLeuLeuLeuLeu 20
Db 57 ATGCAACCCAGAGGCGCCCGCCCTCCCGCAGCGGCTCCGGGCGCTCTGCTGCTGCTG 116
OY 21 LeuLeuGlnLeuProAlaAAspSerAAspSerAAspSerAAspSerAAspSerAAsp 40
Db 117 CTGTGAGAGCTGCGCGCCCGCGAGCGCTGATGATGATGATGATGATGATGATGATGATG 176
OY 41 GlnLeuAArgGlnAArgGlnAValAAspLeuTyrAAsnGlyMetCysLeuGlnGlyProAla 60
Db 177 CAGCTCCGCGAGAGAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 236
OY 61 GlyValProGlyAArgAAspGlySerProGlyAlaAAsnValIleProGlyThrProGlyIle 80
Db 237 GGAAGTCTGCTGCTGCAAGAGAGGAGCCCTGGGCGCAATGCAATTCGCGATACCTGATC 296
OY 81 ProGlyAArgAAspGlyPheGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100
Db 297 CAGGTCGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 356

QY 101 SerTTPth-ProAsnTyrIysGlnCysSerTSPserSerLeuAsnTyrGlyIleAspLeu 120
 DB 357 TCTTGAGACACCACTACAGAGCAGTGTTCATGAGTTCATTAATTCAGCATAGATCTT 416
 QY 121 GtLVsIIAlAGluCysThrPheThrIysMetArgSerAsnSerIleLeuArgValIleu 140
 DB 417 GGGAAATATGGAGAGTACATTAACAAGATGCTTCAAAATAGTCTCTAAGAGTTTGG 476
 QY 141 PheSerGlySerLeuArgLeuIysCysArgAsnIleCysCysGlnArgTTPTrPheThr 160
 DB 477 TTCAGTGGCTCACTTCGGCTAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTTCACA 536
 QY 161 PheAnGlyAlAGluCysSerGlyProLeuPro 171
 DB 537 TTCATGAGAGCTGAATGTTCAAGACCTCTTCCC 569
 RESULT 47
 LOCUS BX299779 641 bp mRNA linear EST 10-MAY-2004
 DEFINITION BX299779 tcay Oncorhynchus mykiss cDNA clone tcay0005D.n.07 5prim,
 mRNA sequence.
 ACCESSION BX299779 GI:42613305
 VERSION BX299779.2
 KEYWORDS EST.
 SOURCE Oncorhynchus mykiss (rainbow trout)
 ORGANISM Oncorhynchus mykiss
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 Procanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 1 (bases 1 to 641)
 GOvoroun,M., Guiguen,Y. and le Gac,F.
 Construction and primary characterization of normalized cDNA
 libraries in rainbow trout, Oncorhynchus mykiss
 Unpublished (2003)
 On Apr 7, 2003 this sequence version replaced GI:29580424.
 CONTACT: Guiguen Y
 INRA - SCRIBE
 Campus de beaulieu, RENNES cedex, 35042, France
 Tel: 02.23.48.50.09
 Fax: 02.23.48.50.20
 Email: Yann.Guiguen@beaulieu.rennes.inra.fr
 Sequence cleaned of vector, adaptor and repetitions. Contact us
 at sigena@portefeuille.inra.fr to obtain the chromatogram of this
 sequence.
 Plate: 0005 row: n column: 7
 Seq primer: M13R.
 FEATURES
 SOURCE
 1.641
 Location/Qualifiers
 /organism="Oncorhynchus mykiss"
 /mol_type="mRNA"
 /db_xref="taxon:9022"
 /clone="tcay0005D.n.07"
 /tissue_type="adipose tissue, blood, brain,
 differentiating gonads, gills, interrenal, intestine,
 kidney, liver, muscle, ovary, pituitary, testis"
 /dev_stage="from embryos to adults"
 /lab_host="MDH10B"
 /clone_lib="tcay"
 /note="vector: pT73D-pac; Rainbow trout multi-tissues -
 normalized + 1 subtraction (tcay) ; Clone distribution :
 AGENAE Resouorce centre. Francois PIUMI,
 Francois.Piumi@jouy.inra.fr, INRA, CRA Radiobiologie et
 Etude du genome (LREG), Domaine de Vilvert 78352,
 Jouy-en-Josas cedex, France, +33 (0) 1.34.65.28.02, +33
 (0) 1.34.65.22.73"
 ORIGIN
 Alignment Scores:
 Pred. No.: 2.09e-76 Length: 641
 Score: 906.50 Matches: 165
 Percent Similarity: 88.35% Conservative: 17
 Best Local Similarity: 80.10% Mismatches: 23
 Query Match: 69.68% Indels: 1

DB: US-10-063-734-122 (1-243) x BX299779 (1-641)
 Gaps: 1
 QY 38 GlnYsAlAGlnLeuArgGlnArgGluValValAspLeuTyrAsnGlyMetCysLeuGln 57
 DB 2 AGAAAGCAGCTTGAACAGAGAGATGTTGAATACAAAAGTACACAGC---TCCCCCGG 58
 QY 58 GlyProAlAGlyValProGlyValArgAspGlySerProGlyAlaAsnValIleProGlyThr 77
 DB 59 GGTTCGGCTGACCCCTCGAAGAGGAGGTAACTCTGGACCAATGGCATCTCCGGAGACT 118
 QY 78 ProGlyIleProGlyArgAspGlyPheIysGlyValIysGlyIleCysLeuAspGlySer 97
 DB 119 CCGTGCATCCCGGGGCGGATGATGATCAAGGGGAGAAAGAGAGTGTGAGTGAAGCTG 178
 QY 98 PheGlnIleSerTTPTrhProAsnTyrIysGlnCysSerTSPserSerLeuAsnTyrGly 117
 DB 179 TTTGAGAGCAGCATGAAACCACTACAGACAGTGTCTGGAACCTACATCATATGGG 238
 QY 118 IleAspLeuGlyIysIleAlAGluCysThrPheThrIysMetArgSerAsnSerIleu 137
 DB 239 ATGACCTGGGCAAAATAGCTGACTGTACATTACCAAGCTGGTTCAAGAGTGGCCCTG 298
 QY 138 ArgValLeuPheSerGlySerLeuArgLeuIysCysArgAsnIleCysCysGlnArgTTP 157
 DB 299 CGTGGCTCTTCAAGCGGCTCCCTGAGGCTGAAGTGAAGACAGCTCTGCCAGCGTTGG 358
 QY 158 TyrPheThrPheAnGlyAlAGluCysSerGlyProLeuProIleGlnAlaIleIleTyr 177
 DB 359 TACTTCACTTCAACGAGAGCTGAGTGAACGAGACCTCTGCCATTCATCATCATCAC 418
 QY 178 LeuAspGlnIleSerProGlnMetAsnSerThrIleAsnIleHisArgHisSerSerVal 197
 DB 419 CTCACCAAGAGAGACCTGAGCTCACTCACTCACTCACTCACTCACTCACTCACTCACT 478
 QY 198 GlnGlyLeuCysGlnGlyIleGlyAlAGluValAspValAlaIleTTPValGlyThr 217
 DB 479 GAAAGGTTGTGTGAGGGGATCCGGGAGGCTGTGTGAGTGTGAGTGTGAGTGTGAG 538
 QY 218 CysSerAspTyrProIysGlyIleAspAlaSerThrGlyTTPAsnSerValSerArgIleIle 237
 DB 539 TGTGCTACTACCCCGAGNAGAGAGCATGTACAGGTTGAACTGTATCCAGGCTCTTC 598
 QY 238 IleGlnIleLeuProIys 243
 DB 599 ATGAGGAGCTGCCCAA 616
 RESULT 48
 LOCUS BQ424201 902 bp mRNA linear EST 23-MAY-2002
 DEFINITION AGENCOURT 7896901 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6159635
 5', mRNA sequence.
 ACCESSION BQ424201
 VERSION BQ424201.1 GI:21119516
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 902)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cga@bbs-remail.nih.gov
 Tissue Procurement: ATCC/DCTD/DTP
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLN at:
 http://image.llnl.gov

Plate: LLM13509 row: a column: 12
High quality sequence stop: 570.

FEATURES

Source

1..902
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6159635"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_72"
/note="Organ: skin; Vector: PCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 2 kb. Library constructed by Life
Technologies."

ORIGIN

Alignment Scores:

Pred. No.:	3..71e-76	Length:	902
Score:	906.00	Matches:	166
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	69.64%	Indels:	0
DB:	5	Gaps:	0

US-10-063-734-122 (1-243) x BQ424201 (1-902)

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QY 78  PROGLYILEPRGGLYARGAAPGLYPHELYSGLYGLULYSGLYGLUCYSLEUARGLUSER 97
DB 3  CCTGGAGTCCCAAGTCGGATGATTCAGAAAGAGAAAGGGGGAATGCTCGAGGGAAGC 62
QY 98  PHEGLUGLUSERTPHPRPAAENYRYLVGGLNYSERTTSPSERSELEUAENYRGLY 117
DB 63  TTGGAGAGTCTCGACACCCCACTAAGACAGTTCATGAGTTCATTGAATTAAGC 122
QY 118 1LEASPLEUGLYLYSILEAGLUCYSTRPHETHRLYSEWECARSEASERALEU 137
DB 123 ATGATCTTGGGAAATTCGGAGTGAATTCACAAAGATGCTCAATATGCTCTA 182
QY 138 ARGVALLEUPHESERGLYSERLEUAARGLEULYCYAARGAANALACYSGYGLNATGTP 157
DB 183 AGAGTTTGTTCAGTGGCTCACTCCGCTAATAATGCAAAATGCATGCTGACGCTTG 242
QY 158 TYRPHETHPHEANGLYALAGLUCYSESGYPROLEUPROILEGLUALLEIETR 177
DB 243 TATTGACATTCATGAGCTGAATGTCAGACCTCTTCCATTAAGCTATTAATTAT 302
QY 178 LEUASPGLNGLYSERPROGLUWETAAANSETRHLEASNLLEHISARGTHRSESERVAL 197
DB 303 TTGGACCAAGGAAGCCCTGAATGAATTCACAAATTAATTCATGCACTTCTCTG 362
QY 198 GLUGLYLEUCYSGGLUGLYLLEGYALAGLYLEUVALASPVALAAILETPVALGLYTHR 217
DB 363 GAAGGACTTTGTGAAGAAATTTGGTCTGATGATGATGATGATGATGATGATGATG 422
QY 218 CYSESERASPTYRPROLYSGLYAASPALASERTHGLYTRPAHSESERVALSERAGLILE 237
DB 423 TGTTCAGATTACCCAAAGAGATGCTTCACTGATGATGATGATGATGATGATGAT 482
QY 238 LLEGGLUGLULEUPROLYS 243
DB 483 ATTGAAAGAACTACCAAAA 500

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RESULT 49

BI763295

LOCUS 603047656F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5188069 5',
DEFINITION mRNA sequence.

ACCESSION

BI763295

VERSION BI763295.1 GI:15754873

KEYWORDS

EST.

SOURCE

ORGANISM Homo sapiens (human)

REFERENCE

1 (bases 1 to 903)
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMNL at:
<http://image.llnl.gov>

Plate: LLM11469 row: 0 column: 14
High quality sequence stop: 875.

FEATURES

Source

1..903
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:5188069"
/lab_host="DH10B"
/clone_lib="NIH_MGC_116"
/note="Organ: pooled colon, kidney, stomach; Vector:
PCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dt primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.:	4..63e-76	Length:	903
Score:	905.00	Matches:	166
Percent Similarity:	98.81%	Conservative:	0
Best Local Similarity:	98.81%	Mismatches:	2
Query Match:	69.56%	Indels:	0
DB:	4	Gaps:	0

US-10-063-734-122 (1-243) x BI763295 (1-903)

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QY 76  GLYTHRPROGLYILEPRGGLYARGAAPGLYPHELYSGLYGLULYSGLYGLUCYSLEUA 95
DB 2  GGTAACCTCGGATCCCAAGTCCGATGATTCAGAAAGAGAAAGGGGGAATGCTCGGG 61
QY 96  GLUSERPHEGLUGLUSERTPHPRPAAENYRYLVGGLNYSERTTSPSERSELEUAAN 115
DB 62  GAAGCTTTGAGAGAGCTCGACACCACTCAAGACAGTGTTCATGAGTTCATTGAAT 121
QY 116 TYRGLYILEASPLEUGLYLYSILEAGLUCYSTRPHETHRLYSEWECARSEASER 135
DB 122 TATGGCATGATCTTGGGAAATTCGGAGTGAATTCATTAAGAAATGCTCAATAT 181
QY 136 ALALEUARGVALLEUPHESERGLYSERLEUAARGLEULYCYAARGAANALACYSGYGLN 155
DB 182 GCTCTAAGAGTTTGTTCAGGGGCTCACTTCGGCTAAATGCAAGAAATGCAATGCT 241
QY 156 ARGTRPYRPHETHPHEANGLYALAGLUCYSESGYPROLEUPROILEGLUALLE 175
DB 242 CGTTGGTATTTTCAATTCATGAGAGCTGAATGTCAGACCTCTCCCATTAAGCTATA 301
QY 176 LLETYRLEUASPGLNGLYSERPROGLUWETAAANSETRHLEASNLLEHISARGTHR 195
DB 302 ATTTATTTGGACCAAGGAAGCCCTGAAGAAATTCACAAATTAATTCATGCACTTCT 361
QY 196 SERVALGLUGLYLEUCYSGGLUGLYLLEGYALAGLYLEUVALASPVALAAILETPVAL 215

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Db      362 TCTGTGGAAGACTTGTGAAGAAATGCTGCTGATTAAGATGTTCTACTGGGTT 421
Qy      216 G|Y|ThrCysSerAspGlyProlysglyAspAlaSerThGlyTrpAsnSerValSerArg 235
Db      422 GGGACTTGTTCAGATTACCCAAAGAGATGCTTCTACTGAGATGAGATTCAGATTCTCTCC 481
Qy      236 l|e|l|e|l|e|g|u|l|e|u|p|r|o|l|y|s 243
Db      482 ATCATATTGAAGAACTACCAAAA 505

RESULT 50
BE387335
LOCUS   BE387335
DEFINITION 688 bp mRNA linear EST 21-JUL-2000
mRNA sequence.
ACCESSION BE387335
VERSION   BE387335.1 GI:9332700
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 688)
AUTHORS  NIH-MGC hftp://mgi.nci.nih.gov/.
TITLE    National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL  Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: sgapbs-remail.nih.gov
          Tissue Procurement: ATCC/DCTD/DTF
          CDNA Library Preparation: Ling Hong/Rubin Laboratory
          CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ULNL)
          DNA Sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/ULNL at: image.lnl.gov
          Plate: LICM284 row: 1 column: 09
          High quality sequence start: 10
          High quality sequence stop: 686.
FEATURES
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            /clone_id="NIH MGC 20"
            /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
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            cloned into EcoRI/XhoI sites using the following 5'
            adaptor: GGCACGAG(G). Size-selected >500bp for average
            insert size 1.8kb. Library constructed by Ling Hong in
            the laboratory of Gerald M. Rubin (University of
            California, Berkeley) using ZAP-cDNA synthesis kit
            (Stratagene) and Superscript II RT (Life Technologies)."
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ALIGNMENT SCORES:

Pred. No.:	1.2e-75	Length:	688
Score:	899.00	Matches:	171
Percent Similarity:	98.84%	Conservative:	0
Best Local Similarity:	98.84%	Mismatches:	2
Query Match:	69.10%	Indels:	1
DB:	2	Gaps:	0

US-10-063-734-122 (1-243) x BE387335 (1-688)

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Db      170 ATGGACAGCCCGAGGCGCCGCGCTCCGCGAGCGGCTCCGCGGCTCTGCTCTG 229
Qy      21 LeuLeuGlnLeuProAlaProSerSerAlaSerGlnLeuProlysglylyleGlnlyAla 40
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Db      230 CTGCTGCAGCTGCCCGCGCCCTCGAGCGCTCTGAGATGCCCAAGGGGAACAAAGCCG 289
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Qy      61 G|y|v|a|p|r|o|g|l|y|a|s|p|g|l|y|s|e|r|p|r|o|g|l|y|a|a|n|v|a|l|l|e|r|p|r|o|g|l|y|l|e 80
Db      350 GGAAGTCCCTGGTTCAGACGAGAGCCCTGGGGCCAAATGGCAATTCGGGTACACCTGGGATC 409
Qy      81 ProGlyAArgAspGlyPheIysGlyGlyIysGlyGlyIysGlyIysGlyIysGlyIysGly 100
Db      410 CCAAGTCGAGATGATTCMAAGAGAAAGGGGGAATGCTGAGGGAAAGCTTTGAGAGAG 469
Qy      101 SerTPThrProAsnTYrIysGlnCysSerTPSerSerLeuLeuTYrGlyIleAspLeu 120
Db      470 TCTGGACACCACTACACAGACAGTGTTCATGAGTTCAATTGAATTATGACATAGACTT 529
Qy      121 G|y|y|s|l|e|a|a|g|u|c|y|t|h|r|p|h|e|t|h|y|s|e|r|a|s|e|r|a|s|e|r|a|l|e|u|a|r|g|v|a|l|l|e|u 140
Db      530 GGGAAATTTGGGAGGTGTACATTTCMAAGATGCGTTCAAAATGTGCTTAAGAGT-TTG 588
Qy      141 PheSerGlySerLeuArgLeuIysCysArgAsnAlaCysCysGlnArgTyrIysPheThr 160
Db      589 TTCAGTGGCTCCTCGGCTAAATGCAAAATGCAATGCAATGCTGTCAGCGTTGTATTTCACA 648
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Job time : 3213 secs